

# FIGURE 1

ACTGCACCTCGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTCGTCTCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAACGCGACGCCCTGCCACCAGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACAGGAGATTGGCGGGAAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCGAGAGCAGCACTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGAGCAGACA  
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT  
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CCGAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG  
AAAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTCTGACGGCTTCGAAGAACG  
GAAGATGCCGTGTGCCGCCGGCAGAGGCTGAAGGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGAAGACCTGTAATGTGCCGGACTTACCCCTAAATTATTCAAGAAGGATGTCC  
CGTGGAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTCTTGGTTGTTCTTA  
AACAGACTTGTATTTGATAACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAACG  
TTGGCCGCCATGGCCAATTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTCAACAAATAAGCATTTCCTGCATTCTAGTTGTGGTTGTCCAAACTC  
ATCAATGTATCTTATCATGCTGGATCGGAATTAAATTGGCCAGCACCATGGCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAAGAACCGAGTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCGAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLP~~RRA~~ALGLL~~PL~~LLLLP~~PA~~PEAAKKPTP~~CH~~RCRGLV~~D~~KFNQGMVDTAKKN~~F~~GGNTA~~W~~EAKTLSKY~~E~~SS~~E~~IRL  
LEI~~E~~GLCESSD~~F~~ECNQM~~E~~AQ~~E~~EH~~E~~LEAWWLQLKSEY~~P~~DL~~F~~EWFCV~~K~~TLKVCCS~~P~~GT~~Y~~GP~~D~~CLACQ~~G~~GSQR~~P~~CSG  
NGHCS~~G~~DSRQGDG~~S~~CR~~CH~~MGYQ~~G~~PLCTDC~~M~~DGYF~~S~~SLRNE~~H~~SICTACDESCK~~T~~CSGLTNRDC~~G~~ECEVG~~W~~VLDE  
GACVDV~~D~~ECAA~~E~~PP~~P~~CSAAQ~~F~~CKNANG~~S~~YT~~C~~ECDSSCV~~G~~CT~~G~~E~~G~~P~~G~~N~~C~~KECIS~~G~~YAREHGQC~~A~~D~~V~~DEC~~S~~LAEKT  
CVRKNEN~~C~~YNTPG~~S~~YVC~~V~~CP~~D~~GF~~E~~TEDAC~~V~~PP~~A~~E~~A~~ATE~~E~~GESPTQL~~P~~S~~R~~DL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

### **FIGURE 3**

CAGGTCCA ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCACGCCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCAGCATGGCCGGAGGAGCGCCTTC  
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCCTGCTGGACTGCAGGGCGGAGGC  
CGGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTACCAGGAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGCTTGGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAAACAGTGCCTCACAGGA  
TCAGTTGTTCAAGTTGGTTCCATGTCTTGGAAAACAGGATGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTAAAATGCTATCT  
TCTTAAAACATGTCAACAAGCTGAGTGCCCAGGCAGGCGGGTGCAGAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTCGAGTGTCCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCCACGATGTATGAATGGTGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACGTGACAAAGCAAACGCTCAACCACCTGCTTAATGGAGGAGC  
TGTCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACACCCCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT  
□ CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGGTGCACAT  
□ GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
□ TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC  
□ ACACGCCCTCACTTAAAAGGCCGAGGAGCGGGATCCACCTGAATCCAATTACATCTGG  
□ **TGA**ACTCCGACATCTGAAACGTTAAGTTACACCAAGTTACAGCTTGTGACTCCTGGCTTAACCTTCA  
□ TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTATTAGCT  
□ TCATTATAAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG  
□ CATGATGGTATAGATTCTTGTTCAGTGCTTGGACAGATTTCAGATTGTCAGATATTAG  
□ TCAGGTTAAAATTTCACTGAGCTGACTTGTGAGTTGGCAGATATTTCAAAATTACAATGCATTATGGT  
□ GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAATGCGTAAGTCACAAGAAT  
□ TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCACTGAGATTGTCAGATATTAGAT  
□ GTTGTGTTACATTAAAATTGCTTTAATTAAACTCTCAATACAATATATTGACC  
□ TTACCAATTCCAGAGATTCACTGAGATTAAACACTGAGCTGAGCTGGCATT  
□ AAACAATATAATATTCTAACACAAATGAAATATAATGTATGAACCTTTGCAT  
□ TGGCTGAAGCAATATAATATTGTAACAAAACACAGCTCTACCTAATAACATTAT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA  
AAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTGGC  
CGCCATGGCCCAACTGTTATTGAGCTTATAATG

## FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094  
><subunit 1 of 1, 379 aa, 0 stop  
><MW: 41528, pI: 7.97, NX(S/T): 2  
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC  
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPVCE  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGCGTCCGGCGGTGCAAGGCCAGGAGGCGGAGGCCAGGCGCGCGGGCCAGCCTGGG  
CCCCAGCCCACACCTCACCAAGGGCCCAGGAGCCACCAATGTGGCGATGTCACACTGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGCCACTTGGCTCTGGGTGCCAGCAGGGTGTGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCCGGAGGGCCGTACTGCCAGGA  
GCAGGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCACTTGGGCGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGTATCTA  
TCCAGTCTTGGGAAACGTACTGGGACAACGTAAACGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTCTGGGGCATGACCCGTGGATGGGGCATTGCTACCGCCTGGGCACCA  
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGTGAACCCAGGGAG  
GTGCTCCACAGCCTCGAGGCTCTGAGAAAGTGGCCAACCTGATTGAGCCTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCGTCTGTGCCCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGCGTCTGATGGTGCCTGGTGGTTCTCGCTCG  
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACGCCACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCGGCCACTCCTGGG  
CAGCCTGGGCGAGAGGGCCACTTCCGATCGCGCCGTCAATGAGTGCACATCGAG  
AGCTTCGTGCTGGCGTCTGGGCGCGTGGCATGGAGGACATGGTCATCACTGAGGCTG  
CGGGCACCAAGCGGGGTCCGGCTGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTCGCCGACAGAGCCCCGGCCAGGCCAGGGCGCTAA  
CCGGCGCGGGTTCCGCTGACGCAAGGCCCTGGAGGCCGGCAGGCCAGGCGACTGGCG  
GAGCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGCTGGGAAGAGCACAGCTGAG  
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCAACTCCGTATTCTTTTTTTAGACAGGGTCTGCTCCG  
TTGCCCAAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCCCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC  
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT  
CCTGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTTCACTGTTAAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADD
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTGGGACACATNACGCCCTGCCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTCGCTGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGATCCGCGCAGTTGCCCTGCACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTCAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGCCCTCCAACCCTCTGCTGCTGTTTC  
CATGCCCTAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTTCCCCCAGGAAGCCTT  
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGAA  
GGACAAGAGTCGACGTGAGTTCCCTGGGAGTCTCCAGAGATGGGCCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTGAGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA

故其後人之為也，則又非其子孫之所能及也。

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQI SSSDT  
DPPADGPSNPLCCCFHGPFASTLNPVLRHLFPOEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

## amino acids 1-47

### N-glycosylation site.

amino acids 31-35, 74-78, 84-88

## Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

### N-myristoylation site.

## Amino acids 56-60

### Amidation site.

## amino acids 70-74

## **FIGURE 10**

CCACCGCGTCCGAAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC  
GACCAGCTGAGCAGGCCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTCAACGGCGTCGCATCTCCGCCACGCCAGGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGGAAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG  
GCTGGTTATGGCCTTCACGCCAGGGGCCGGCCAGGCTTCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGGCCCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAAGCAGAAGCAGTCAGTTGTGGCTCCGCCAGGCCGGACCAAGCGCACAC  
GGCGGCCAGCCCACGTAGTCTGGAGGCAGGGCAGCAGCCCTGGCCGCCTCCC  
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCAGGGGAGCCAGATCCCC  
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGAGGGCAGGCCGGTG  
CCCCAGGGCGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC  
CGCTGAAAGGTCAAGCACTGAAGGCCCTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCAGGCCAAACTCCTCCTGGCTAGACTGTA  
GGAAAGGGACTTTGTTGTTGTTGTTGAGAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGCCAGGCCCTGCACCCACCCCCACTCCAGCCC  
CGGAATAAAACCATTTCTGC

## FIGURE 11

MGAARLLPNLTLCLQLLILCCQTOYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTCAACAGAACCCCATCCAGT  
CATTGGATTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTC  
AAAGTCTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGT  
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACA  
TGGATTCCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTCAGAGTTCTCCATTGCAAGGAAAC  
AATATTGACACCATTTCACGGGCTGCTTGCCTAGCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCTATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTTGACGGAACCTCCTGACCAACAAGGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTCAATTGTAATTGCTGTCC  
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCGAT  
AAACACATTCTTGACAGCCTCTCAAATCTGCTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTGATAATCTCTCCAAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCTTGGTTTGTGACTGAGTATTAAATGGGTACAGAAATGGCTCAA  
ATATATCCCTCATCTCTAACGTGCGGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCGTCAGGAAATTAAATATGAATCTTGTCTGTCCACCACGGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACACGCCCTCAAACCTTACACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTTGTAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA  
CAAACACTCACATGGGTAAAATGGGCCACAGTTAGTAGGGGGCATCGTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTGTTCAGAGGC  
CACCAACCATGCCCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGCTTGCTCAGCGTCTTGTGCTGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATAACCGGGGCGGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACACTCCATCCTGGAGATGACAGAAACAGTTTCAAGATCGTCTCCTAAATAACGAT  
CAACTCCTAAAGGAGATTCAAGACTGCAGCCATTACACCCAAATGGGGCATTAAATTA  
CACAGACTGCCATATCCCCAACAAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGCGGACAATTAGACTCTGAGAA  
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT  
TTGTGCATTGAATACTCTGTAATTATAACGGTGTACTATATAATGGGATTAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGTCTTTAAATCTT

## FIGURE 13

MGLQTTKWPShGAFFLKSLLIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPaelHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSSPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARRELNMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTTSLPTIPDWDGRERVTPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKGHSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLUVL  
LSVFCWHMHKKGRYTSQWKYNRGRKDDYCEAGTKKDNSILEMTETSQIVSLNNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGGCGGCGGAGACAGAGGGCAGAGGGAGAAGCTGGGCTCCGTCTGCCTCCACGAGCG  
ATCCCGAGGAAGAGCCGCGGCCCTCGCGAGGCGAAGAGGCCAGAGGAAGACCCGGTGGCTGCGCCCTGCC  
TCGCTTCCCAGCGCCGGCGCTGCAGCCTTGCCTCTGCCCTGCCAGGGCAGGGAGGGTACGTGGAGGTCCATCT  
GCTTCTGCTGATCCTCGACAGATCGCCTCTCCCTGCCAGGGCAGGGAGGGTACGTGGAGGTCCATCT  
CTAGGGCAGACACGCTCGAGCTCGAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TGGTTTCATCATTGAGACGCTCGAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCTTGCACATTCTGGACATTGGTCTGTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCAGGGTGGAGCGTGTCAAGAGGATGCGCATTGTCCACGG  
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGGGGGCCGGGGCTGA  
GGGAGAATGTGCCACGGGTACATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTGCATTGGTGTGGGCCAGGTAGACTTCACACCTTGAAGTCCATTG  
GGAGTGGCCCCATGAGGACCATGTCTCCTTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCGTGTCC  
AGAAGAAGTTGTGACGGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
GTCATACGTCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGGACTTGCAGAACATCCAGGATCTG  
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCAGGTGGACTACTGTGCCCTCAGAAAACCACGGATGTGAAC  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCCTCAGAAAACCACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAAACAAACCGGCTGTGAGCATTGAGTGCCTCAGAACATGGAGGAGGCT  
ACTACTGCCGTGCCACCGTGGCTACACTCTGGACCTGTGTGAGCAGTGGGACTTCTCAGTGCCTCAGAACAGGCTTCC  
AGCAGGACCATGGCTGTGAGCAGTGGGACTTCTCAGTGCCTCAGTGCAGTGGGACTTCTCAGAACAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGTCTCCGGTGGATTACTGCCTGTGAGTGGGACTTCTCAGAACAGGCTTCC  
GTGTCAACATGGACAGATCTTGCCTGTCACTGTCTGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAATTGGACTCTTGTCTCTGGGACCACTGGTGTGAACATTCTGTGTGAAGCAGTGAAGATTGTTGTG  
GCCAGTGCCTTGAAGGTTATATACCTCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGCTGCCAAGCTATA  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGCAGACTCATACAGTGCAGTGGCTGTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCGAACACATTGTGTTA  
ATAATGGGAACTCTACATCTGAAATGCTCAGGGATTGTTCTAGCTGAGGAGCAGGAAGCGGTGCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGCTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTGAGGTG  
TGAAGCAGTTGTCACTGGAATTATAGATTCTTGACAAATTCCCCAAAGCCGCTCGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTCACTCTGAGAAACTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCC  
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGGCCATTGTTCACTGACGGGCTCAGGATG  
ACGTCTCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTTGAGGACTTCTATGCCAGCACAATGG  
AGGAGGAACATACAAGAGATTGCCCTGAGGCCACAAACAGCATCTTCTATGCCAGACTCAGGACTCTCCAG  
ATGAGATAAGTAAAAACTCAAGAAAGGATCTGAAACAGGATCTGTGAAGCTAGAAGACTCCGATGGAGACAGGACTCTCCAG  
CAGGGGAACGTCCAAAACGGTCCAACAGCCAACAGAAATCTGAGGCCAGTCACTGAGGACTTCTATGCCAG  
CCTGTTCTAATTGGCAGTGCACACAGATATCTGTTGAGAAGACAATCTTACGGCTACACAAAGCTT  
CCCATTCACAAACACAGTCAATGAAAGGGCTTGGAGAAAACACGATCAATGAAATGAAACCTTATAATGT  
TCAGAACCTTGCACAAAGGAAGAAGTAAAGAAAATTAAACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGGCC  
TGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATCGCACATTGTTAGTCATTGATCAGGATTACAAT  
GAACGAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAACAAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTAACTAATTGTTAAATTTATCTAGGAAAAAAATCCT  
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTGAAATATACTGTGGACAC  
AACTTGCTTCTGCCCTCATCCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAGTTGCAAGTCTTACCT  
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGACTGGACTTTACCTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGACTTGTGGAACAAGTGGATTAAATACAATATTAAAATTCAACACTTCAG

## FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRIHARTHPTALLESSCENKADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLREN VPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAI VGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVQKKLCTAHMCSTLEHN  
CAHFCINI PGSYVCRCKQGYILNSDQTT CRIQDLCAMEDHNCEQLCVNPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG  
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQCFC EGYILREDGKTCRRKDVCQAI DHGCEHICVNSDDSYTCECLEGFR  
LAEDGKRCR RRDVCKSTHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKCTEGPIDLVF  
GSKSLGEENFEVVKQFVTGIIDS LTISP KAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEELQEIASEPTNHLFYAEDFSTMDEISEK LKKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINI QDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTORMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGCTCCCGCGCACGCTCCGCCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCGCCAGGGAGGGC  
**CATG**ATTTCCTCCGGGCCCTGGTACCAACTTGCTGCGTTTTGTTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGGGGCCAGCTGCAACTGCACCTGCCGCCAACCGTTGCAG  
GCGTGGAGGGAGGGAAAGTGGTCTTCAGCGTGGTACACCTGCACGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCGCTGGAGGGTCTCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTCAAGACAAACAAGGCAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCTA  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCTTAGATGTCATCCGTG  
GGTCTTAAGCCTACCAACCTTCGCTTCCATGGCTGGAGTCTATGTCGAAGGCCAC  
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTGTGGAGCTGTTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCGCCGGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGGCCCTCCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTGGCTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**  
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC  
CCCCTTGATCTGACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAAATCTC  
TTATTAAAACATGAAATATGTGTTGTTTCATTGCAAATTAAATAAGATACTAA  
TGTTTGTATGAAAAA

## FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCACTGCGGCCACCGCCAATGAAACGCCCTCCGCTCTAGTGGTTTTCCACTTG  
TTGAATTGTCCTATACTCAAATTGACCAAGACACCTTGTCTCCAAATGCAAATGTGA  
AATACGCAATGAAATTGAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTG  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTCCATT  
TAGATAATGTCGTATACTGCAAATATTAAATAAAACTTTAACAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGTACAAGAAGTCTAGAAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAATATTAGCTGAATCATCTCATTACTAGGTTACAAGAACACA  
CTATCTCAGCCAAGGACACCCTTCTAACACTCTTACTGAATTGTAACAGGCTGAAT  
AATTGTTCAAAGGGATACTTGTAGTTGGACAAGTTCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACTCATGCACACTGTTGAAACAAGCTACTTTAACGGATATAGCTCTCAAAGTTTCTTGTGAT  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTGTGAT  
TCATAAACATGAAACATATTCTCCTCATATGAATATGGATGGAGACTACATAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGCTTCAGTCAATGAGCTCAAACCC  
AGAGTATTGGTCTTGTGATCATCTGACAACCTTCTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTCAGTAATTTCAGTCAATGAGCTCAAACCC  
ACCCACATTATGAACCTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCAATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTGCAATTGATGTCCTCTGGCTTCCATTGGTATTAAGATTATAATTTC  
TTACAAGGATCACTCAACTAGGAATAATTATTCAGTGAATTGCTTGCATATGCATT  
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAAATTCAAACAAACTAATAAGCTCT  
TAGCCTATTCTGCTGAACCTGTTCTGTTGGATCAATACAAACTAATAAGCTCT  
TCTGTCATTCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTTATCTCATTGTTGGTGTCACTACAACAAAGGGATTGGCA  
CAAGAATTTCATCTTGGCTATCTAACGCCCAGCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACACAAAGTATGTTGGCTAGCACCGAAAACAACCTTATT  
TGGAGTTTATAGGACCATGCCTAACATTCTGTTAATCTCTGGCTTGGAGTCAT  
CATATACAAAGTTTCGTCACACTGCAGGGTTGAAACAGAAGTTAGTTGGCTTGGAGAACA  
TAAGGTCTGTGCAAGAGGAGCCCTGCTCTGTTCTGTTGGATCTAACAGTCAAGGAACT  
GGGGTTCTCCATGTTGCAACGCTCAGTGGTTACAGCTACCTCTCACAGTCAGCAATGC  
TTTCCAGGGGATGTTCAATTCTGTTGTTGGATGTTAAGGTAACATAGAGAATG  
ATTACAGATTGTCAAAATGTCCTGTTGGATGTTAAGGTAACATAGAGAATG  
GTGGATAATTACAACTGCACAAAATTTCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCCAAATTAAACTACTAGACAAAAGTATTAAATCAGTTTCT  
GTTTATGCTATAGGAACTGTAGATAATAAGGTAATTGATCATATAGATATACTATGT  
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAGATATTGGAAAGTAATTGGTT  
CTCAGGAGTGAATACTGCACCAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA  
TGTCTGAAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC  
CCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA  
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAAATGAACTGTTTTCTGTAGAC  
TAGCTGAGGAAATTGTTGACATAAAATAAGAATTGAAAGAACACATTTCACCTTGTGAA  
TTGTTCTGAACTTAAATGTCCACTAAAACAACTAGACTCTGTTGCTAAATCTGTTCTT  
TTCTAATATTCTAAAAAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 19

MKRLPLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVEYRNSVTDSLSDPTDIITYEILAESSLLGYKNNTISAKDTL  
SNSTLTFVKTVNNFVQRDTFVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFKQTTEFDT  
NSTDIALKVFVFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF  
WNYSPDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSSGSPSIGIKDYNILTRITQLG  
IIISLICLAICIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL  
LHYFFLAAFAWMCIEGIHLYLIVGVYINKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCTTGTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC  
TGGTTCTTCAGTCAAAGCACCAGGA

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## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGAGGGAGTTCCCCGAAACCCGGCCG  
CTAACCGAGGCCTCCCTCCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA  
CAAGAACGCCGCCGCTGCCCTGCCCGGGCCGGGGAGGGGGCTGGGCTGGGCGAGGCAGG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGTGCAATCCGATAAGAAATGCTCGGG  
TGTCTGGCACCTACCCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCGCGTCAGAGCAGGAGCGCTGCGTCAGGATCTAGGGCACGACCATCCAAACCC  
GGCACTCACAGCCCCCAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCGCCGGGCCCCCTGCCTCTCGACGCCGGGCC  
CCACGTGCACTACGGCTGGGGCACCCCATCCGCCTGCGCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTCCTGCGCATCCGTGCCAGGGCGTCGTGGACTGCGCCGGGGC  
CAGAGCGCAGCAGTTGCTGGAGATCAAGGCAGTCGCTCTCGCGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGCAGTACCTCTGCATGGCGCCGACGGAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAACCGCCTCCGGTCTCCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG  
CAGAGGCTTCTCCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTCTGCCCTGGAGACCGACAGCATG  
GACCCATTGGCTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAAGTAAC  
GAGACCATGCCGGCCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCAGTCCAGTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCCTATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATACCTCCATCGATGGGGAC  
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTTAATTTCAGGAACAGGTGATCCACTCTGTA  
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGGAGTCCACTCTGTA  
AACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATATCTACTTCCAGGG  
ACCATTGCCCTCCAAATCCCTCAGGCCAGAACCTGACTGGAGCAGGCATGGCCACCAG  
GCTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGCCCTGGACAATTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTTGCTGTCCGGTGTACCTGC  
TTCCATCTCCAGGCCACCAGCCCTGCCCCACCTCACATGCCCTCCCATGGATTGGGGCCT  
CCCAGGCCCTTACATTGTCAACCTGCACTCTGTTCAAAATCAGAAAAGAAAAGAT  
TTGAAGACCCAAGTCTTGTCAATAACTTGCTGTGGAGCAGCGGGGAAGACCTAGAAC  
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTCTTACATTATTATGCCCTAAATTATTTATGTATGTAAAGTGGAGTTG  
TTTGTATATTAAAGGAGTTGTTGT

## FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSQLCMGADGKMQGLLQYSEEDCAFEET  
EIRPDGYNVYRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTLGAEVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

100 200 300 400 500 600

## **FIGURE 23**

CCCAGAACGTTCAAGGGCCCCGGCCTCTGCGCTCCTGCGCCGGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTCTGCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGGCTATTTAGCCTGCAAAACCCAA  
AGAAGACTGTTCTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCCTGTGAAGGCCGCAATT  
TGTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTGTGGCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCTGTAATCCAGCAGTTGGAAAGG  
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCAATATGGTAAACCCCC  
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA  
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## FIGURE 24

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIILLENPRLGSQST  
NSSYTMNTKTGTLQFNTVKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIIAAVVVA  
LVIISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCCCGACCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTCAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTCTCTCCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGTTCTATGGCATTCA  
TTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTACTGACTG  
TGGAACTCTTAAGGGCCCATTACATTGAAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCTATGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTATGTACGTGTGAAATCAGGCTTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGAAATGATTAGGTCTTTAACTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTACAGACTAACATATTGAAAAATTGAATACTCCACAG  
ACTTCCAGTAAACCTTACTGGCTGGATTATCTAAAACAATTATCTCAGTCACCAAT  
ATTAATGAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTG  
ACTGCCTGAAAAATGTCGAGCAACTACAAGAACTCTATTAATCACAAC  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCTACATAATCTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCAATTATCAGAACTAAAGACATGAACCTTAAGCCTCTTATCA  
ATCTTCGCGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTAAAGTACCCATGT  
TGCTCTCAAAAGTTGAAATCTCAAATTGGATCTAAATAAAATCCTATTAGAA  
TACGAAGGGGTGATTAGCAATATGCTACACTAAAGAGTTGGGATAAAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAAATAGAAGC  
TACTAACACCCTAGATTGCTTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCTGGTACCTGGACTCTG  
CCAAACCTCAAGGAAATCAGCATAACACAGTAACCCATCAGGTGTACTGTGTCATCCGTTG  
GATGAACATGAACAAAACACATTGATTGCTGAACTGGCAGATTCACTGTTGCGTGGACC  
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTCTCTAATCTAAATGTTAGAAGCTGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAAACCTTGCCTAAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA  
GATATAATGGCGTAACCTCAAAGAAGGGGTTATATACTGTATAGCAACTAACCTAGT  
TGGCGCTGACTGAAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG  
GCTCTTGAATATTAAGAGATATTCAAGGCCATTCACTGGTGTCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCCACCATCTCAGAAAAACAGAAAAAA  
TGTGTAAATGTCACCAACCAAAGGTTGCACCCGATCAAAAGAGTATGAAAAGAATAATAC  
CACAACACTTATGGCCTGCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACTGTGATGGGGACACAGCTATGTGAGGAATTACTACAG  
AAACCAACCTTGCAATTAGGTGAGCTTATCTCCTCTGATAAAATCTCTGGGAAGCAGGAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTACCAACAAATATGTCCT  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKKVDCCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNAKIEYSTDGPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKTELPEKCLSELNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINRSLVIAGINLTEIPDNAVGLENLESISFYDNRL  
IKVPHVALQVVNLKFLLDNKPINRIRRGDFSNMLHLKELGINNMPPELISIDS LAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC  
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

GCCTGGACTGGCGAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**ATGAATCT**  
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCAAAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACACCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGAAAACGTCCGTGTTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGTTGGCTGGTTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGT**A**TAGTGTCCAATGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCACTAGAAATAAGTGGTTACTTCTCCCATTGAAACATTGAA  
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT  
AATTAAAAGCAAATAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCASNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRFL  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCATCCTCCTGCTGGTGCT  
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCCGCTGCGAGTGCTCCGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGAGCAGTCCCCGAGGGCATCCCACCGAG  
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGCGCCGTGGAGGCCGGCG  
CCTTCAACAACCTCTCAACCTCCGGACGCTGGTCTCCGCAGCAACCGCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCGCGCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCCTGTCACCGCTGTGCC  
CATCGCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC  
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCAACCTCTCCTACAACCCATCA  
GCACCAATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGCAGCTGGCGTGGAGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCAAGCTGACCAACTGGAGGAATCAGTCTTCACTCGTGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGGCTCCTGTGGTGTTCGG  
CGCCGCTGGCGCTCAACTCAACCGGCAGCAGGCCACGTGCGCCACGCCAGTGTCCA  
GGGCAAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTTCACCTGCGGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGGACGAGGGCACACGGTGCAGTT  
GTGTGCCGGCGATGGCACCAGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGTGATCGCCACGCCATGGCTTCATCTTT  
TCCATGCCGCCACCTGCATGTGCCAGCTACTGCCGACTGGCCCCATCAGCCAACAA  
GACCTTGCCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGGCCACTG  
TGCCTTCCCTCGACATCAAGACCCCTCATCATGCCACCCATGGCTTCATCTTT  
CTGGCGTGTCTCTGCCCTGGTGTGCTGTTCTGGAGGCCGGCAAGGGCAACAC  
AAAGCACAAACATCGAGATCGAGTATGCCCCAAAGTCGGACGCAGGCATCAGCTCCGCC  
ACGCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGGGGGCAGGGACCCCCCG  
GGCGGCCGGCAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCCAGTCTTCCACCTC  
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCCCTGCTGCCCG  
CCAGCCCTACCACCTGCCCTCTTCTACAGGACCTCAGAAGCCCAGACCTGGGGACCCCA  
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA  
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATTT  
TATGAAAACTTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELLENENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVEISH  
WPYLDTMTPNCLYGLNLTSLSIHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLFNNSGNQLTLEESVFHSVGNLETLILDSNPLA  
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCCCACCGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTCGCCAGGCCAGCC  
AGGGAGGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCCTCGCTCTGCTCCTGC  
TGTTCGCCTGCTGGCGCCGGCGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGCACCCTGGCTCAAGTCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTCTACTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT  
ATAAAATCTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACAG  
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCAAGCCATCATCGTGGATCGGGCTTCATTGTCTTCTGCTG  
CTCATCATGCTCATCTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCCAGCGGACACGCCATCATCAATGAGGCG  
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATCTAGAGGCGCCTGCCACTTCCTGC  
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCAATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAAACA  
AACAAAAAAACA

## **FIGURE 32**

MGAPAASLLLLLFAACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELYSISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIHQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFFFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTAEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 33

GGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTTCTCCTTCCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCGTGGCAGCAGGATGGTCGCTG  
TTACTTGTGATGAGATCGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTCTTGCCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTTACCATTTATTCTGCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTCGTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTCTGGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCTACGCCAAC  
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGCTTGGAAAACCGAGTGGATTCTAGTCTCCGGGCCCTG  
CCCAAGAACAGAACCTTGCTCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTACCCCTGCCCTGGGGCTGCGACTGGCACCACATCCCAGGGTGGTTAAAGATGAAC  
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGACTTGTGGATTACAAGA  
ACCTCATTCTGGATCTGGCAACAATAACATCGTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGGA  
GAAATTGCGGGGCTGCAAACACTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGGACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAACTG  
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGCA  
GAACGCTTGGGTCGAAAGTGTGATGAGCAGCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGCGGAGACCGGGACGCAC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCGGACTGCTGCTGG  
GTTGTCACCTCCGCCTTCACCGTGGCATGCTCGTGTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGAGACGAGATGCCAACTCCCGCGTCCGAGATTAATTCCCTACAGACAGTCTG  
GACTCTCCTACTGGCACAAATGGGCTTACAACGAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAGGG  
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG  
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCCT  
GACCCCTTACTTAGCTCCCTCTGAAACAAAGAGCAGACTGTGGAGAGACTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGGCCCTTGACAGAAAGCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCCGGTTCTATAC  
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACCTTGACTTCTGAC

## FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLEVILNDNLISTLPANVQYVPITHLDLRG  
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLAPPQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNQIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDIECPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLLLVFVTSAAFTVVGMLVFLRNRKRSKRRDANSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCCCTGTCGCGGCCATAAGGGAAACTGTTGGC  
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGGTCGTCGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG  
AGAATGAGGCCGGCGTTCGCCCTGTGCCTCCTGGCAGGCAGCTCTGGCCCGGGCCTGCTACAGCCTGC  
CGGCGAACACCCCCACTGCGACCGTGTGGCTGCTGGCCCTCGGGGCTGCTACAGCCTGC  
ACCAAGCTACCATGAAGCGGCAGGCAGGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCCTGCGTGCAGGGCGAGCTGCGCGCTGTGCTCGCCTCTGCGGGCAGGCCAGG  
GCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCAGTCCCAGT  
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGTCCTCGACCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCAACGGCGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGTCGAGCCCGAGGCTGGAAAGGAGATGCGATGCCACCTGC  
GCGCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGTCCTGCGCCGCCGG  
GCCGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA  
TCGCGGACGAAATCGCGCTCGTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTGGGAGG  
CTTGCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCGCTCTGTGACCA  
GTGGGAAGGACAGCCGACCCCTGGGGGACGGGGTGCCACCAGGCGCCGCCGGCACT  
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCCCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT  
CGACTCCTCCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTGTGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAAAGCCCTCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCCTGGAGAGTGATCCTGAGGCCGCTGTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTTGCAGGGAGTCCCTCTGGCTCTAGTGATGCAAGGAAACAGGGAA  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC  
TTGTGTAACTGACAATTCTGCAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGATACTGGGGACCGGGTAGTGCTGGGAGAGATATTTCTATGTTATTGGAGAA  
TTTGGAGAAGTGAATTCAAGACATTGGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAATGTTCTATGTTCAAGGCTAGGAGTAT  
ATTGGTTCGAAATCCCAGGGAAAAATAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVIFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR  
KESMGPPGLESDEPEAALGSSSAHCTNNGVKVGDCDLRDRAGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGATTCA  
CGTCAGTCAGACGGCACCATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGTATC  
CCCCGGCTACCTGGGCCCGCCCGGGCGGTGCGCGTGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGTGGGTGCGGA  
GGGGCGTGTGCCGGCGCGCCGTGGGTGCAAACCCCGAGCGTCACTGCTGCCAATGA  
GGGGCGCGAAGCCTGGCGCCACTCTGCCTGCTGCTGCCACCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTTCATGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTCCGGCTTTAAAAC  
CCCCAAGTGGCAGACCGGGATTACCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC  
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCACCTGCACCAATTGTGTCTGAGAGAAATGAACCTCTTATTCA  
TTTATCAGACTTAAGTTAACATGCAGATGGTTATTGGTCACTACATATTCA  
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACACATTCCCTGTAACCACGGTTAAA  
ACCCACCGTGGCCTTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGA  
CTTGTATTAGCCGGACTGTTATCACAACCATCACTCGCGATGGAGTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATT  
CAGCAGGCGGG  
CAAGAACATGAGTGCAGGCTGACTGCGTCTGCAAGCAGTGCCTCTCCTCAGAACAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCTGGATGCC  
TTAAAGATCTATGTTCT  
TCTCA  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT  
TGCGCTGCTGTCAGAGGAGCAGCTATGATTGGAAACCTGCC  
ACTTAGTGC  
GGTGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAGCGTTATTATACATCTGTAAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCA  
AAAAAAAGATTTAGAAGTGC  
AAATTTAGT  
GTTATTGTTCACCTCAAGCCTTGC  
CC  
GAGGTGTTACA  
ATCTGTCTTGCG  
TTTCTA  
AATCAATGCTTA  
AATAAAAT  
TTTAAAGGAAAAAA  
AAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESNDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGGCTGGGGCGGTGCGCTTCTT  
CCTTCTCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACCTTGGAG  
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGCCCTCGGGTGGCTACGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGCACTGTGACTGCCAAGCGGCTACGGGGTGAGGCCGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCCTAGGCTGCATGGGGGCAGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA  
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAACAGCAGTTGGTGGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGGTCAACGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTGTCAAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACTGTAGGACCTCCTCCCACCCACGCCAGCTGCCCTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGGAGAGTGGGTAAGCACCCTACCTG  
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTTCAACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT  
TCTGTGTTACCAACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPPIWLQSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPAGTERPCGGYGGCEGEGRGGSGHCDCQAG  
YGEACGQCGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKA CLGCMAGPGRCKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQI PESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIFKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCCAGCTGAGCTAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCACTCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCCGG  
CATGGAGCAGCGGCTGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCGTCTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCCGCGCAGGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCGACAGCAGGCTCCAAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC  
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG  
CTCAGGGCAGTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGCTT  
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCCGAGGCCCTGGCCTTCAAGTGGC  
CGTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGCGCTCGTGCCTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGAGGGTACCGAGGAGAGCTG  
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTGGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTATTCTTATTACTGCACTATATTCTAACACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC  
TGGATCTGGCTAAAGTCCTCCACCACACTGGACCTAACGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTATTCT  
AAAA

## FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCCRQPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCAGGAGTCCTCGGCGCTGTTGTCAGTGGCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG  
CATTGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTCCCCGTGGAGTGAAGTTGACCA  
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCA**ACTGGTATCACCTCAAGTCCGTACACGGGAAGACACTGGGACATAC**  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCAACGAA**ATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT**  
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATA**ACTGGAGAATACA**  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAA**ATGCTGCGCATGGAAGCT**  
GTGGAGCGGAATGTGGGGT**CATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT**  
CTTGGTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCC~~TGGTGT~~**GACCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT**  
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGA**ACTTGTAA**  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTGAGCTGGTTCTGGCTCTTCTGTACTGAC  
GACCAGGGCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTGTGG  
TGATGACACTGGGGCCTTCCATCTGGGGCCACTCTCTGTCTCCATGGGAAGTG  
CCACTGGGATCCCTGCCCTGCTCCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAAC**TTGAAGCCAAAG**  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAA**ACTGGAGGCTGGCGCAGTGGCTACGCC**  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAA**ACTCCAGCTCAAAAAAA**

## FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGIFTKSVTREDTGYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTCCCACCCACCAAGTCCAGTGCCGACCAAGTGGCTTATGCGTCCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCCTATGGGTTATTGCAGCTGCTGCCGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTTGTGCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC  
CTCGCTGCCCTGAGGACAAGCAACTGCCACCAACCGTCACTCACGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGTGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAACGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCQKGQC PPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASILVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCACAGCGTCCGGTCTCGCTCGCTCGCAGCGCGGGCAGCAGAGGTGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGTTTCTTGAAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAAGTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA  
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTGTGATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTTAAACTT  
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTGTC  
GCCACCCGGCCTTGTGAGCGTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG  
TTCCAGCAGTGACCCCTGACTTGTGGTGGTAGACGGCGTGCCGTATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGCCCTGTGGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTCGGACAACCCGTACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATGCCACTGGGT  
GTTGTTCTTAAGAAACTGATTGATTTAAAAATTCCAAAGTGTGCTGAAGTGTCTTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTTCTTGTGGTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTTAAAGNAAAAAA

## FIGURE 48

MYHGMMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACCGCGTCCGCTCCGCCCTCCCCCGCCTCCCGTGCCTCGGTGGCTAGAGA  
TGCTGCTGCCCGGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCACCGCCGT  
AGCGCCCGAGTGTGGGGCGCACCCGAGTCGGGCATGAGGCCGGAACCGCGCTACAGG  
CCGTGCTGCCGTGCTGGTGGGGCTGCCGCCGACGGTCGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA  
TAAAGTCATTACTCCATGATACTCTCGAAGACTGAACCTTGAGGAAGCCAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT  
CACAAATTAGGAACTGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAATTCTTGCATATTCTGATGAGAACCCAGCAGTCCT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAACAGAAACACAG  
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTGAATCTGCCCTACAT  
CCTAATCCCCAGCATTCCCTCTCCTCCCTGTGGTACCAACAGTTGTATGGGTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCATC  
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAACATTCTCGAGTGTGTT  
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGGACCCCCACGTTGGCTATCCTTAT  
CCCAGCCAGTCATCCAGCTCGACCTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTCTGCTCTACAG  
CAGCACATATTATCATAAGACAGAAAATCCAGAACATTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAACAAAATCAAATAAGA  
GCAGGAAAAAA

## FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELTPVLPETQEEAKKTFKESREAALNAYILIPSIPLLLL  
VTTVVCWVWICRKRKREQPDPTKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGTAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT  
GTTGCCTCCTGCAGCCTCAACCGGAGGGCAGCGAGGGCTACCACCATGATACTGGTGT  
GTTCAAGCATGCGTTGTGGACCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACACGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT  
GCAGCAAATGTTGCCTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAACCCATCATCAT  
CCACACTGATGAAGCAGATTAGAAGTCTGTATCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTGATAAAAGTGGACTCTTCATCCTCCT  
GGACAACGTGGCTGCCAGCAGGACACAAACCTCCAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCTGGGATTTGACCAAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCAACGGGAAGGAGCAGGTGCCAGAGGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTATACAATG

## FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTAACATACTTGCAGCTAAAACCTAAATATTGCTGCTTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTGATCCTT  
GCCATTGACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGCCTGGTGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCCCAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCATCCA  
ATCAGTCAGTTGCACAGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAACAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGCTGGCTGACGGCCCTGGCATTGCAAGGGACCGTGGAAAGTGA  
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAACCCATTCA  
GGATTGCCCTCTGGCCTTGGGAAAGAACACCTGCAACCAGATGAAGAACACGTGGTC  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTGTGATGACAACGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGTGGGAAGTCCCTCTCCCTCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGGCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGCAGCACAGATTTGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA  
CCACCTTCCTATGTCCTCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT  
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTGTCCTGTTCTGAAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAAATTGGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC  
TATGTGTTCAA

## FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVQCQGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDWTVECEDPFDLRLVG  
GDNLCGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC  
CCACCGCGTCCCGCGGACCGCGTGGCGGACCGCGTGGCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG  
CGTCTCGGCCTTCCGGCTGCTGCAGTGGTGCAGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCACCTCAGGGCTGGCAAAGAAATGTGCAAAAGTCTTATGCT  
GCGGGTCTAAACTGGTGCTCTGTGGCGGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTACCTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG  
CTGTCTCGTGCCAGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTAAGCCTTCAGCCTCATGGCCTCCAGGG  
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAACGAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT.  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCACTCTAG  
AGTCGACCTGCAGAAGCTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

## FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA  
KLVLICRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

## **FIGURE 58**

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKKVKEIGDVSILVNNAAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEOKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

### Signal sequence:

## amino acids 1-19

## cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

### Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

### N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCACCGCGTCCGGACCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC  
AGGGAGGAGCACCGACTCGCCGCACCCCTGAGAGATGGTTGGTGCCTGGAAGGTGATTG  
TTTCGCTGGCCTGTTGATGCCTGGCCCTGTGATGGCTGTTCGCTCCCTATACAGAAGT  
GTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTT  
TTCCCAGCTCAGATACAGCCAGAACGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCCTTATGTTGTACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTACTGATGATACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGATTATACAGTGCACTAATTCAAGTTCCAGATATTCCTGAATATAAAAATA  
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA  
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT  
TGTGGATGAGAAGCAAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT  
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAGTACTTGCAGAGA  
AGATACAGTACAGTCAGTTAAGCCATGGTTAAGTGAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTACCCATGACCAGCCTGAGAGCTTGACATGATTAATCGA  
TTCATTTATGGAAAAGGATGGATCCTTATGTTGGAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCTTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAGTGAGC  
TTTGTGTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA  
AATTTAGGGCTTGAATAGGAAGTTTAATTCTTAAGAGTAAGTGAAGGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCCAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAAGTAAAAAA

## FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSQPLFLTPYIEAGKIQKGREL  
VGPPGLNMKSYAGFLTVNKTYNSNLFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRO  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGKWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTCGGCTCCGGAAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT  
TTTCCCTTCTAACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGTACAGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCGAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTTCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAAGACTGGGTTAGTCCTAACATCAAATTGACTGGCTGGG  
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTAACGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAATTTAAAAAAGCAAGTATTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAACAGGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCAGAAGGAGGGAGACTCACAGAGCTAACACCAGGATGGGACCCCTGGGTC  
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGAAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTCTCAGTGGCTGGGTCTGGCTGGCCCCCAGCAGCCGGC  
ATGCCTCAGTTCACTGACCTCCACTCTGAGAATCGTACTGGACCTTCACCAACTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGCTATAAGCTGACAGGA  
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCCAGAAGAGGACAACAAGTCTGTTACCCG  
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCCACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTTACCCAGGGGTCTGCA  
AGCTGCTGGGCTGGATGACCTCTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACAGGGCACCATGTACGGGTGATTGTGCGCTTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCGTCCA  
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGCTACTTCTCACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTACACCTCACGCATCGCCG  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCTGCCCTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCTGCAGGCTGTTACCTGGCCAAGCCTGGGACTCACTGGCC  
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG  
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCTTCCATCCGGGCCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACAGGGCGAGGGCAACCTGGAGCTCACTGGC  
TGCTGGGGAAAGGACGTCCAGTGCACGAAGGCGCTGCCCCATCGATGATAACTTCTGTGA  
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAAGAGTCTATGAGTTCACTGCTCCAATGCC  
ATTCACTCCTCAGCAAAGAGTCCCTTGGGAAGGTAGCTATTGGTGGAGATTAACTATAG  
GCAACTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAAGAAGGGTTAATTTGTG  
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCACCAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL  
YQGVCKLLRLDDLFI~~VEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY~~  
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKDQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGCGCTGAGTGGGACTGGAGTGGAAACCGGGTCCCGCGCTTAGAGAACACGCGATGACCA  
CGTGGAGCCTCCGGCGAGGCCGACGCTGGACTCCTGCTGCTGGTCTTGGGCTCTGGTGC  
GCAGGCTGGACTGGAGCACCTGGTCCCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGAGGATTCCACCTCTGGATCTTGGGCTCCATCCACTATTCCGTGCCCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGCTTGAAACACCCCTCACCACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTGGAACCTGGACCTGGAGGCCCTCGCCTGATGGCCGCAGAGATCG  
GGCTGTGGGTGATTCTCGCTCCAGGCCCTACATCTGAGTGGACCTGGGCTTGCCAGCTGGCTAC  
TCCAAGACCTGGCATGAGGCTGAGGACAACCTACAAGGCTTACCGAAGCAGTGGACCTTATTTGACCACC  
TGATGTCCAGGGTGGTGCACCTCCAGTACAAGCTGGGGACCTATGCGGTGCAGGTGGAGAATGAATATG  
GTTCTATAATAAGACCCGCATACTGCCCTACGTCAAGAAGGCAGTGGAGGACCGTGCATTGTGGAACTGC  
TCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGGATTGTCCAGGGAGTCTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCAGGGACTCAGGCCAAGATGGTGTGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCTCACAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCACGGAGGCCAACATTGGCTTCATGAATG  
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCGACTATGACTATGATGCTGTGACAGAACGCCGG  
ATTACACGGCCAAGTACATGAAGCTTCAGGACTCTCGCTCCATCTCAGGCATCCCTCTCCCTCCCCCACCTG  
ACCTCTTCCAAGATGCGTATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTGGACGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCACACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCACGTGATGTCAGGGGGCAGG  
TGTTGTGAACACAGTATCCATAGGGATTCTGGACTACAAGACAAGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGGGAGAATCTGGGGAGTCAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTCAACCTCTGAAAACCTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAAGGGTTGGCCTGGACAAATGGNGTCTCCCTCCAGAAACACCCACATTACCTGCTTCTCTGG  
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGGTTGTATTCA  
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTATCGTTTGAGGGAGACGATGGCGGGCCCTGCATTACAGTTCACGGAAACCCCC  
ACCTGGGAGGAACAGTACATTAAGTGAGGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCGCTC  
CTCTTGACCTGAAGCTGGCTGCTGCCACCCCTACTGCAAACAGCATCTCTTAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCTTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGC  
TGGCTTGTTGATGATGGCTTCTACAGCCCTGCTCTGTGCGGAGGCTGTGGGCTGTCTAGGGTGGGAGC  
AGCTAATCAGATGCCACGCCCTGGCCCTCAGAAAAGTGTGAAACGTGCCCTTGACCGGACGTACAGCCC  
TGGCAGCATCTGCTGGACTCAGGCCTGCTTTGCTGGTCTCTGGGAGGCTGGCCACATCCCTCATGGCCCC  
TTTATCCCCGAAATCTGGGTGTGTCACCAGTGTAGAGGGTGGGGAGGGGTGCTCACCCTGAGCTGACTTGT  
CTTCCTTCACAACCTCTGAGCCTCTTGGATTCTGAAGGAACCTGGGCTGAGAACATGTGACTTCCCT  
TCCCTCCACTCGCTGCTCCACAGGGTGAAGGCTGGGAGGACATGTGAGTCTGGCAGAACGCATGGCC  
CAAGTTAGCAGGTGTCTGGTCTCAGTGGAGGAGGACAGCTCACATGTGAGTCTGGCAGAACGCATGGCC  
CATCCAGGGAGGAGGACAGAACAGGCCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCC  
AGGGAGGAGGAGAACAGAACAGGCCCAGCTCACATGTGAGTCTGGCAGAACGCATGGCC  
GGAGGGACAGAACAGGCCCAGCTCACATGTGAGTCTGGCAGAACGCAGGGGAGGAGAACAGCAGGG  
ACAGAACAGGCCCAGCTCAGTGGCCCCGCTCCCCACCCCCCACGCCGAACAGCAGGGGAGGAGAACAGCAG  
GAAGTGTCTCAAGTCCGCATTGAGCCTGTTCTGGGCCCCAGCCAAACACCTGGCTTGGCTCACTGTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PARTLGLLLL VVLGFLVLRRL DWSTLVPLRLRHRQLGLQAKGWNFM LEDSTFW  
IFGGSIH YFRV PREY WRDR LLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFT EAVDLYFDHLM SRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDNKG DLSKGIVQGV LAT  
INLQSTHELQLTTFLFNVQGTQPKMVMEYWTGWFDSWGGPHNILD SSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTA KYMKL RDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSF GYI LY  
TSITSSGILSGHVHD RGQVFVNTV SIGFLDYKTTKIAVPLI QGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSPKLN FRIYS LDMKKSFFQRFGLDKWXSLP EPTPLPAFFLGSLSIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTL YLPGPWLS SGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACCGGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGTCCCAGGACC  
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGCTGCCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGTTGCTAGTGGATAGGGTCACTGACCGGTTCTCCTAGACGGGGCC  
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTGTGTTGGGCCAC  
CGGCTTTGAAGATGCCATGGAGCGGCCAACGCCATACAGTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGTCTATACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTCAGAG  
TGGGAGATGGGGGTCTCCATCCTGGTTGCTCGAAAACCTGAAATTCAAGAACCTC  
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCCGTGACTGCTAGG  
AGAAAAGATCTGCTCTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCGTCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTCCTCCGATTACTACCAAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCTTGGGACCTTACCTCCCCGAGCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGGCCCGTGGCCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGATGGATGGGTGTTCCAGGGTGTGAGCGAACATGAG  
AGACAAACTATTTGACGGGAAACTGGGTCAAACACTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGTCTAACAGCAGTGACTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGCAAACAACTCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTCCCTCCAGTTGCAAAATGCCATATCCTCAAGCTCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTACGTGCAAGATCCTGCTTTCTAGGGGAGCCTCAACAAAATT  
CATTGCTGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCAAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATAACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGGACTGAAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCAGTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTAAACCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG  
ATGGTGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTIILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTTGAACACGTCTGCAAGCCCCAAAGTTGAGGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTATCTGCCCTACACTCTTCTGGTTATTCAGGATACCTTGAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT  
GCGTTCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGTTAGTGAAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGTGTATTTGCTCAAAA  
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACCTGGAT  
TTAAAGTCCAATAACATTGCAACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTTATTACCATGTCA  
AAAACTTGGAGTCACTTATTTCTCTAACAAACAAGCTCGAACCTTACAGTGGCAGTATT  
AGTTTACAGAAACTCAGATGTTAGATGTGAGCTACAACAAACATTCAATGATTCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG  
TGGAAAGATCACCTTTGATAACCCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGTGCAGGAAC  
AACTTCCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTTAAGTCATTCAACATTCAAATCATTGTTTTTTCTTTGGGG  
AAAGGGAAAGGAAAATTATAATCACTAATCTGGTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPAKIPIAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMGLESLRELRHLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLSLKKMMNVAELELQNCERIPIHAIFSLNSNLQELDLKS  
NNIRTIEEISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTGACATTCCATTCTGGTACAAACTGACTTTTTATTTCT  
TTTTTCCATCTCTGGGCAGCTTGGGATCCTAGGCCCTGGAAAGACATTGTGTTTACACACATAAGGAT  
CTGTGTTGGGTTCTTCTCCTCCCTGACATTGCATTGCTTAGTGGTTGTGAGGGAGGACACGTGG  
GCTCAGTGCTTGCTGCACTTATGCCTAGGTACATGAAGTCTTGACCTACAGTGATTATGCCTGTC  
ATCGCTGGTGTATCCTGGCGCTGCTCCCTGCTGATAGTTGCTGCTGTCTTACTC AAAACACAAAC  
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGGCTGTA AAAAATCACAACCCAGACAAGGTGTGGGGCAAG  
AACAGCCAGGCCAAAACCATTGCCACGGAGTCTGCTGCCCTGCAGTGTGAAGGATATAGAATGTGTGCC  
AGTTTGATTCCCTGCCACCTTGCTGCTGCGACATAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGACAGAAAGGACACAG  
CTCCCCATCAGTTCATGAAAATACTCAGTGCTGGAAACAGCTGGAGTCTGGAGATCCCTACAGAGAGCTC  
CACTGGGGCAACCCCTCAGGAAGGAGTTGGGGAGAGAACCCCTACTGTGGGAATGCTGATAAAACAGTC  
CACAGCTGCTCTATTCTCACAAAATCTACCCCTTGCGTGGCTGGAACGTGAGTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGTCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT  
AGAAGGCTCATGCCATTGACCCCTCTAATTCTCCTGTTGGGGAGCTGACAATGGGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCTATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGAAAGTGAACATTAAGCTTTGACGGAACCTCAGCAATGGGCCCTGCTGAGCTT  
CAAGTCTGAGTAAAAGCACTATGTTCTGTTGAAATCATCAGTACATTGACGTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGCTTTGTTCTACTACTTCTCTCTAACATCTCTATTCCAAACTGT  
GGCGTTACCTGGATACCTTGGAGGATCCTTCAACCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
TGTGTGGCACATACAAGTGGAGAAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAAATAGAC  
AAACAGTCCAAATTGATTTCTTGCATCTATGATGGCCCTCCACCAACTCTGGCTGATGGACAAGTCTG  
GGCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT  
TACCGGGGATTCTGCTCCTACACCTCAATTATGAGAAAACATCAACACTACATCTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTAACTCTAAATGGGATAACTTGCAACTAAA  
GACCCAACTTGAGACAAAATTATCAAATGTTGGAATTCTGCTCCCTTAAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCATTACACCAATATAATCACCTTCTGCATCCTCAACTCTGAAGTGTGATCACC  
CGTCAGAAACAACCTCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAGTCAAATGCACTGGCAAAATATAACACCAGCATGGCTCTTTGAATCCAATTCA  
TTTGGAAAAGACTATACCTGAATCACCATATTATGTTGGAATTGAAACCAAACCTTTGTTCAAGTTAGTCTGCAC  
ACCTCAGATCCAAATTGTTGCTGTTCTGATACCTGTAAGGCCCTCCACCTCTGACTTGCATCTCCAAAC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTGTGAAAGGTGATCCCTTATTGGACACTATGGGAGA  
TTCCAGTTAACATGCCCTTAAATTCTGAGAAGTGTGAGCTCTGTTGATCTGAGTGTAAAGTTGATATGTGAT  
AGCAGTGACCAACAGTCTGCTGCAATCAAGGTTGCTCCAGAAGCAGGAGACATTCTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGCAAGTGCAGTGGCAATTCAAGGATTTCTG  
GAAACACATGCCAGAAAACCTCAAACCCAGCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTG  
AATGTGGTACTGTAGCGACAATCACAGTGGAGGATTGTAATCAACGGGAGACTACAAATACAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCCCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTGAAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGCATGTA

## **FIGURE 70**

MELVRRLMPLTLLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSEDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVRSRKRDISSYKWKTDSIIGPIRLKDRSASGNQFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGC CGCG  
GGACATGCGCCCCAGGAGCTCCCAGGCTCGCGTCTCCGTTGCTGCTGTTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACCGCGTGCACCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAGTTCGGCATCTTCATCCACTG  
GGGAGTGTTCGCCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCAGTTCAAATATGAAGAT  
TTTGGACCACTATTACAGCAAAATTTTAATGCCAACAGTGGGCAGATATTTCAGGC  
CTCTGGTGCAAATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTTGTTGGGGT  
CAGAATATTGCGGAACGGAAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACCTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTTCATCCGCTCTCCTTGAGGATGAATCCAGTTCAAGCGGCAATTCCAG  
TTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATTCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGATCAAAACTGGAACAGCACAGGCTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTTGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA  
CATAAAATGGAAAATGCATGACAATAGACAAACTGTCTGGGCTATAGGAGGGAAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG  
GAGGAAATCTTTGATGAATATTGGGCCACACTAGATGGCACCATTCGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTCCTAAATGGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAAC TG  
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC  
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTATGGCAGTTCAGCCCTTCCCTTTCCACTA  
AATTTTCTTAAATTACCCATGTAACCATTAACTCTCCAGTCACCTTGCCTAAAGTC  
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACGTGAAAATTATGTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAAACTGTAAAATGGTGACCTGTATAGGGCACTTACCCAGGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAA  
GTTTTCTTCTTCAATTATAAACATAAGTGTACTGTAACTTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAACATAAAACTCATTGTGCAA  
ATGTAA

## FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYI  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTCCATCTGGACCACGAGGCTCTGGTCCAAGGCTTTGCGTGAGAAGAGCT  
TTCCATCCAGGTGTATGCAGAATTATGGGATCACCCCTGTGAGCAAAAGGCCAACAGC  
AGCTGAATTCACAGAACAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTTGAGCTATGGCTGGGTGGAGA  
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTGGGTG  
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT  
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCAACAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAGAACATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTGTGTCACAGAAGTTTATGAAACTAGCACCATGTCTACAGAAC  
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAACATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTGCTCTCTTGGTGTGAGCTGGTCTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTACAAACAAAGAACATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCTGGAA  
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCAGCTGGGAAATCAAAGGGCCAAGAACCAAAGAACAGAAAGTCCACCCCTT  
GGTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAC  
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTCCACGGCC  
TTCTAGCCTGGCTATGCTTAATAATATCCCACGGAGAACGGAGTTTGCAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTGAAAGAGAACACGTATCCCACCTGACATGTCCTCTGAGCCCGTA  
AGAGCAAAGAACGGCAGAAAGTTAGCCCCTGAAAGCCATGGAGATTCTCATAAACTTGAG  
ACCTAATCTCTGTAAGCTAAAGAACATAGAACAAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAACACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAAATTCTATTCTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTCTTCA  
GTTTGATATTCTAGCTTACTCTTCAACTAATTCTTATTCTGCTGAGACTAATCTT  
ATTCTATTCTCTAATATGGCAACCATTATAACCTTAATTATTATAACACACCAAG  
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCATTAAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAATT

## **FIGURE 74**

MARCFSLVLLLTSIWTRLLVQSLRAEELSIQVSCRIMGITLVSKKANQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVISRISPNSPKCGKNGVGVLIWKVPVSRQF  
AAVCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTGGTGCCGACTTCACGATGG  
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGCCACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCATTGGATTGTGGAGTTCTTGCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCAAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTGTAGA  
TGGGAAAACAAGAAGGATAAATAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGAATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGTTCAGTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC  
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG  
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCACCCCAAGGACTCTTGCTTCAAGCCCTCTGGCTCGTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTGTGGGATTGAGAAGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTTGAGGAGAAACCCCTGGACTTCAC  
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNI PEEQPVASTPTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTGAGGAGCTGCCTGGGACGTTGCCCTG  
GGGCCAGCCTGGCCGGTCACCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCCA  
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTAACACGGTTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTATGCCAAAGACCTCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGCCAGAGAGAAGGACGTGCTGGTGGCATCGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGCCGAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTTACCGCTGGCTGGCAGATC  
ACGGCGCTACCAACTCCACGAGGCCAGCAGGTCTGTGAGGCAGGCTGCCGGTG  
GTGGCCTCCTTGAGCAGCTCTCCGGGCTGGAGGAGGGCCTGGACTGGTGCAACGCCGG  
CTGGCTGCAGGATGCTACGGTCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGGTGGC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTCTTGCCGCCTGGAAGTTCCATGCCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCTGTGGTTACCCGCATCCTAACTGTGGCCCCAGAGCCTGGGT  
CCGAAGCTTGGCTCCCCGACCGCAGAGCCGCTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGCCCTCCCTGCCGATTCCCTACTGGCTGTATTATTGAGTGGTT  
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTCTCAATTAAATTCT  
TTAACATTTTTACTATTTTGTAAAGCAAACAGAACCCATGCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTTGAGGCTTCTG  
GAGGGTTCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGGCCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCC  
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTCCAGGCAGGAAATCTGAGGGAAGGAAGAAACTCCCTCCCT  
TCCCTCTGGTCAAAGAATCTGTTGTGTCATTGTTCTCCTGTTCCCTGTG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTCGCAA  
AA  
AA

## FIGURE 78

MGLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGGTGGATCGGCACACCGCAGCAGCGCA  
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCAGGGCGTGTGG  
GTTGGGAGGAGCTCGCAACGCCACCTATGCCACTACGCCCGGTGAAGAATTGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGGCGTTCCGGTGGC  
CGACCAAGGATGGGACTCGATGGCACTCGAGAGGAGCTGACAGCCTCCTGCACCCGAGG  
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGTA  
CTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCC  
CTGGTGAAGCCAACCAACCTGCTGCACGAGAGGCACACGGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCCTGGTAATTGAAACATGTTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG  
ACAATGACCGGAGGAGGGGCCGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC  
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCA  
TAGTCCCAGAGGATAAGCAATA  
CTATTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCATAGACTGAAACTCCCCT  
GGCCCCAGCCCTCTCCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGGCCGGACCTTGAAAAA  
AAAAAAAAAAAAAA

1000 900 800 700 600 500 400 300 200 100

## FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRSLKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTCCGACTCGGGCGAGCCGGTGGATCTGAGCAGGTGGAGCCCCGG  
GCGGGGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCTGTTGTCGCTCCAG  
CCTGTCGTCGTCGTTGGCGCCCCGCTCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTCGCTCGATTGCGCCGAGGCCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCGTCGTCCTCTCCCTGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT  
GAGGAGGTGACGCGGGGCCTCCGCACCCCTGGCCTGCCCCATTCTCCCTCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCAGCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCCGGGGCCCGGGCAGGGAGGCCCTCCATTGCTATCACATG  
TTTACCAAGGGCTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT  
GGTCTGCTCTTCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG  
CAATAAAGATTGTAAGCAGACATTGCAATTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTTAATTACAGAAGAATTGGTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA  
GAAGGACCACATGTGGCCTGTTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA  
AAACTTACATCAGCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGG  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACTGGTACATTGTTGACAAGGCTGTCTG  
CGGAATAATGGCTCTTCTTACACATGCCAAGTGGTGGCACCACAAAATACGTAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAAGACCTGTATAACT  
CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCTC  
ATGCTGAAATTGTTCCAACATAGCAAGACTTTGAAATCTGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCACTCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGG  
GATGCCATTCTTCACTGTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTTGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTAGAATCCAGCAAT  
AATGGTAACATTGACAACGTAAAGAAAAAGTACAAGGGGATCCAGTGTAAATTGTATT  
CTCATAATACTGAAATGCTTACTGATCAGATACAAACTATTAAGTATGTCAAC  
AGCCATTAGGAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCAACCATGCCTACTAAATGTACAGATATGCAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

## FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCDKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFIAKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRMLMELFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCCGCGCTCCCGCACCCGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGCGGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCACCCTGCTGTGCCTGC  
TGCTGGCGGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGGACCTCGGCTCCAGTC  
AAGCCGGCCCGGCTCTCAGCTACCGCAGGAGGAGGACCCCTCAATGAGATGTTCCGCGA  
GGTGAGGAACGTGAGGAGGACACGACAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT  
ACAATGAGACCAACACAGACAGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGCTTTACAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGAGCAGAAGGAGGCCACGAGTCATCATCGACGGAGGACTGTGGGCCAGC  
ATGTAACGCTGAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACAGCTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAACAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGGAGGGCGA  
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTGTGCCAGTGGCTCCCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTCATGGAGGAGGTGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCTGCCGCTGCCGGCT  
GCACTGCTGGGAGGGAAAGAGATTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTTCCCCAGGTGTGCTTAAAGCTGACAGCATGAGGTGTTGCAATTGTCAGC  
TCTCTCCAGTAAGTTCCCCCTGGCTTGACAGCATGAGGTGTTGCAATTGTCAGC  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACATGTGG  
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTCAGGCTGGCTTGCACATCAA  
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTCCATGGGATAGGTAAGCTG  
TGCCTTCAGCTGTCAGATGAAATGTTCTGTCACCCCTGCATTACATGTGTTATTCTAC  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCAGCACAGCCTGGGAGGGGTCAATTGTTCTCCTCGTCATCAGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGAGCAGTTCAT  
CTGGTTGTACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCCACAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTCTTGAGGCATGCACATCTGGAAATTAAAG  
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT  
TGCATTAGTAATTGAAAGGTATATGACTGAGCGTAGCATAAGGTTAACCTGCAGAAACA  
GTACTTAGTAATTGAGGGAGGATTATAATGAAATTGCAAATCACTTAGCAGCAAC  
TGAAGACAATTCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTCCAGAGTTCTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGATAAACATAAGTTGCATTAGAAATCAAGC  
ATAAAATCACTGCAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDQ  
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDECGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASCAGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVHQELEDLERSLTEEMALGEAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTCAGCCCCTCCACTCTCCCTCCAAACACACATGTGCATGTACACACACACATA  
CACACATACACCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGGCTAGAAAAGGACAC  
TAAAGCCTTAAGGCAGGGCTGGCCATTACCTCTGAGCTCTTGGCTTGTGAGTCAAAAACATGGGAGGG  
CCAGGCACGGTACTCACACCTGTAATCCCAGCATTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAGGAG  
TTCGAGACCGCCTGGCAACATGGAGAACCCCCATCTCACTAAACAAACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCAGCTACTCAGGTGGCTGAGCCAGGAGAACATGGCTGAATCCAGGAGGCGGAGGATGCAGT  
CAGCTGAGTGACCGCTGCACTCCAGCCTGGTGCAGAAGACTCTGTCTCAAACAAACACGGGAGGA  
GGGGTAGATACTGCTCTGCAACCTCTTAACACTGCACTCTTCCAGGGCTGCCCTGATGGGCGCTG  
GCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAACGGCATATTGAGGAGGGCAAGAAGTACGCCCCG  
GTGAGAATGACTGCCCTGGGAGGGTGGCTTGGGAGGGCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCCCTGCCCCCTGAGCTCCACCATGAGGCTTCTCGTGGCC  
ACTCTGCTAGCTGGTGGCTGGTGCACACTGCCACTGTGCCCTGAGCTGGTACCCCTGAGTGTCCCCCTGCCCCCTCA  
GTGCGCTGCCAGATCGGCCAGCTGGTATACGCCCGCTGCTCTACCGCGAGGTACACTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGCACTCCCCGCAAGGACACAGACCCCTGCTCTGAGAGCAACAGCATTGT  
CCGCTGGGAGCAGAGTGAAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTGG  
TGCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGACCGGGCT  
GGAGGACACAGCTTGCAAGGCTGGCCAGCTACAGGAACCTATCTAACCAACACAGCTAACCGCATCGC  
CCCCAGGGCTTCTGGCCTCAGCAACTTGCTGCCCTGCAACCTCAACTCCAACTCTGAGGGCATTGACAG  
CCGCTGGTTGAAATGCTGCCAACTTGGAGATACTCATGATTGGGGCAACAAGGTAGATGCCATCTGGACAT  
GAACCTCCGGCCCTGGCCAACCTGCGTAGCTGGTCTAGCAGGATGAACCTGCGGGAGATCTCCGACTATGC  
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCTTCTATGACAACCAACAGCTGGCCGGGTGCCAGGGGACT  
GGAACAGGTGCCGGCTCAAGTTCTAGACCTAACAGAACCCGCTCCAGCGGGTAGGGGGGGGACTTTGC  
CAACATGCTGACCTTAAGGAGCTGGACTGAACAACATGGAGGAGCTGGCTCCATCGACAAGTTGCCCCTGG  
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGCTCTCATCCACCCCCCGGCCCTTCCA  
CCACCTGCCAGATGGAGACCCCTCATGCTAACAAACACGCTCTAGTGCCTGACAGCAGACGGTGGAGTC  
CCTGCCAACCTGCAAGGAGGTAGGTCTCACCGCAACCCCATCCCGTGTGACTGTGTCATCCGCTGGCCAATGC  
CACGGGCACCGTGTCCGCTCATCGAGCGCAATCCACCCCTGTGCGGGAGCCTCCGGACCTCCAGCGCCTCCC  
GGTCCGTAGGTGCCCTTCCGGAGATGACGGGACTGTGCTGATTGCCGGACTGGCGAACCCGAACCCGAGATCTACTG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGATTGCCGGACTGGCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGCTCTGACTGACACCTGCCATGCAAGGAGGTACCCGGTGTACCCGAGGGGACCT  
GGAGCTGCCAGGGGTGACAGCAGAACAGGGCTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTGTGGGGCTGCTCTCTCCAGCCAGGAGGGACGAAGGACAGGGCTGGAGCTCCG  
GGTCAAGGAGACCCACCCCTATCACATCTGCTATCTGGGTCAACCAACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCTCCCTCCGGGCCAGGGGCCAGCTCTGGCCGCTGCCCTGGGAACCCACAGCTA  
CAACATTACCCGCTCTCAGGCCACGGAGTACTGGGCTGCCCTGCAAGTGGCTTGCTGATGCCACACCCA  
GTTGGCTGTGATGGGCAGGACAAAGAGGCCACTCTTGCCACAGAGCCTAGGGGATGTCCTGGCTCAT  
TGCATCCTGGCTCTGGCTCTGGCAGCTGGCTAGCGGCCACCTGGCACAGGCCAACCCAGGAA  
GGGTGTGGTGGGGAGGCCCTCCAGCCTGGGTTCTGGGCTGGAGTGCCCTCTGTCCGGTTGT  
GTCTGCTCCCCCTGCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCTCAGAAGGGAGACACTGTGCC  
ACCATTGTCTAAAATTCTTGAAGCTCAGGCTGTTCTCAGCAGTAGAGAAACTACTAGGACTACTTTTACCAA  
AGAGAACAGCTGGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTGAGGGCTGGCAGCTGGC  
CAAGACAGATGGGGCTTGTGGCCCTGGGGTGCTCTGAGCCTTGAAAAGTTGCGCTAGAGCCTCTGCCCTCC  
CCTCTGCTGCCAGGGCTCTGGCTGGCTTGCTCTGCTCTGCTCTGGGCCAGGGCTGAAGGGCCACTCCATCTC  
TCTTCTCTGTACAGTCTCAGTTGCTTGCTCTGCTCTGGCTCTGGCAAGGGCAGATCTGAAGGACATTGG  
CTGGGGCTGCCCTCAATGTGGAGGTGACCCAGGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA  
CGCTCATCTCAGCAGCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGAATTGGTACCTTGTGGAGAA  
ATGTGTCAACCTCCCCAACCGATTCACTTTCTCTGTAAAAAATAAAATAACAATAAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNPNRLSFIHPRAFHLPQMELMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADETKTVSVVGRALLQPGGRDEGQGLELRVQETHPYHILLSWTPNPTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGRRPLPPAWAFWGSAPSVRVV  
SAPLVLPWNPGRKLPSSGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

## FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFVDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQNLNNNEWTLKLRQRLTKNAQDKLELHLFMLSGIPDVTVDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENRLALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIOPHSIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVQLQSLPSRVGELETNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGTGCTGGGCCTGAACGCAAGGAGCTGTATTGACT  
GGCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGGGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC  
CCCTTGACAGTGATCTCAAACACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCGGGGGT  
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGCTCTCCTGGGACCTTACCTGT  
ACAGCATGTCTTCTCGAAGACAAGGCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCAGCTCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGGCCACCTAGTTGTCTTGTAGCGC  
CACGTGAGACACCTACAACGAGATGCCAGCTCATGAATGCCCATCAGAAAGAA  
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG  
GGTGCAGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTTCTGCTTCTAAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWPYLYSMSLLEDKGLAEVSKVAEQVNAVNGLYRE  
ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## FIGURE 91

GGCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTGCGCATCGTGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTCGTATCGAATATCTATCTGAGCCTCGTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGTCACCTGTCACCTACACTAAACACATCCAGCCCCTGTCTCCAG  
GCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCGCTTCGGTACTCAGGTGGACCCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG  
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTCTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAA

故其後人之為也，則又非其子孫之所能及也。

## FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAAHCFETYSSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVIIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTGCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGAGCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGCCCCGGCTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAATGTGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG  
CTCTCCTCAATACGGAAAATACCTGACCCTAAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCCTCCACACGGTGCAAAATGGCTCTGGCAGCCGGAGCCCAGAAGTGCCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGCTGAGTTCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCTTGGCCCCCATGTGGACTTTGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCCTCTGTGATCCGTAAGCGATACAACTGACCTACAAGACGTGG  
GCTCTGGCACCCAGCAATAACAGCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCTTCGGGCAACTTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTGGACACACAGGGCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTACAGTAGCCCTGGCCGATGAG  
GGACAGGAGCCCTCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATCTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTCGGGTCTCACCCGTCTCTGCCCTCAGGTGACAGT  
GGGGCGGGTGTGGTCTGTCTGGAAAGACACCAGTCCGGCCCTACCTCCCTGCCCTCCAG  
CCCCTATGTCACCACAGTGGAGGCACATCCCTCAGGAACCTTCCCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCACCTGCCACATCCAGTACTTTCAATGC  
CAGGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGGTCAGCAACAA  
GAGGTGCCATCCATGGGTGTCCGGACCTGGCTCTACTCCAGGTGTTGGGGGATCCTA  
TCCCTGATCAATGAGCACAGGATCCTAGTGGCCCCCCCTCTGGCTTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTC  
TGGATGAAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCGTTAACAGGC  
TGGGGACACCAACTCCCAGTTGCTGAAGCTGGAGTTCACCCTGACCCTTCCTATC  
AGGAGAGATGGCTTGCCCCGTCCCTGAAAGTGTTAACTAGCATTTTGGAATGCCCTCCCTGG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCTAACCCGTAAA  
TGCTGTGAGCTTGACTTGACTCCCAACCCTACATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCTTAGATTCCCTCAATAAGATGTTAACTAGCATTTTGGAATGCCCTCCCTCCGC  
ATCTCATCTTTCTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAAGACTCTGTGCACTA  
TTTCACTTGATATTCATCATCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGCTTTTATG  
GCCTTCCATCATAGTTGCCCACTCCCCTCCCTACTTAGCTTCCAGGTCTTAACTCTCTGTGC  
ACTACTCTTGCTCCCTCTCTCATCAATTTCTGCTCTCATGGAAATGCTGACCTCTCATTGC  
TCCATTTGAGATTTGCTCTCAGTTACTCATGTCCCCTGGAAACAAATCAGTGACA  
TCTACAACCATTACCATCTCAAAATAAGACTTCTATCCAAATAATGATTGATACCTCAA  
TTGTAAAAAA

## FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTL ENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLLPGAEFH YVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GGCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGC  
GGGCTGCTCGCGCGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTCCTCTC  
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGAAACCCACTTG  
GCCTGCATACCGCCTCCCTGTCGCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCTATGCCAATGG  
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCGAGTGGCTCCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA  
ATTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCTGAACTCAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGCCAGGGTCTGGTCTAT  
TGGTTATGACAATGACCGACCAAGGCAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACAGCAATGCGATGCCAGCCAGGGGCCAGGGTCTGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAACGCGAAAAATTATTGGCATTTTCAGG  
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAGAACACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGGTCCCTCTGGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC  
AAATTGTTTTGTCTTGCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTTGAAAATG  
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG  
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTGACATA  
CAAGAGATATGAAAAA

## **FIGURE 96**

MAGIPGLLFFLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGRTETQVGIYILSSSGDGAQHRDSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACIHDGKTYVK  
TQKLRVGFLKPKFDGGRGANDSTSAMPQMKFQWIRVKRTHVPKGWIKGNANDIGMDYD  
AQQPGASGSGVYVRMWKRQQQWERKIIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICY  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAAGCC**ATGGTGGTT**  
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCAGGGTTGTGGCGGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGCTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCCTGGGTGGAGC  
CCCACCCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCCCTGCCATCTGCCTACCTGATGCCCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC  
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTT CCTATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTCGCGACCGCTCTGGTGGAGAAGATCGTCAAGGGGTGCA  
GCTCCCGGGCGCCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC  
CCCGCGCTCC**TAGGGCGCAGCGGGACGCGGGCTGGATCTGAAAGGCGGCCAGATCCACA**  
TCTGGATCTGGATCTCGGGCGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCTCCAAGGCATCAGGCCCGCCAAACGGCCTCATGTCCCCGCC  
GACTTCCGGCCCCGCCGGCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT  
AGGTATTTGTAACCTGCCACATATCTTATTATTCCCAATTCAATAATTATTATT  
CTCCAAAAAA

## FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAACFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICL PDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC  
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHR SWEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTCACATGA  
GATGGGACGAGGAGCTGGCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGAGAACATCTGTCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCAACGAGCGTAGCACTACACGCAGGTGGTATGGCCAAGAACAGAGGAGTC  
GCAGCCCAGGCCAGATGTGCCTGCACTACACGCAGGTGGTATGGCCAAGAACAGAGGAGTC  
GGCTGTGGTCCCACCTCTGTGAGAACGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACCTCCCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAACGTAGGGCCATCCTTCCGGCGACTGA  
AGCATCAGACTCTAGGAAATGGTACTCCTTCCCTAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGCAACCAAGGCTCTGCCTGCTGTGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC  
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGAACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCAAAGATGTCCCTGACAGGGGCAAG  
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTGCCTCCAGTG  
AGGTCTTGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGCACACCTCCTCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCCTGCCAGGTGAGGCTCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCTGGGA  
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTGAATGGGATACCAACTCAAAGGG  
TGAAGAGGTCACTGCCTCTGTCACTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAAGGAAAGGCTACGGGCATGTGCCTCATCACACC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC  
TTTGAGTGGGGAGGCAGGGACGAGGAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAA

## **FIGURE 100**

MHGSCSFLMLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSPLSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSIDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPVWGPPLLGLLLPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTAACCTGAAGTCAGGCTTTCAATTGGGAAGCCCCCTCAACAGAATTGGTCAATTCTCCAAGTTATGGTGGACGT  
ACTCTCTGTTCTCCCTCTGCTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCA  
CAAGGCAAGTTCATGCCACCTTCAAAGCCTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAGTCTGGCAAATATTACACTTCTCTTGGCTGGAAACAGGATTGGTAAATACTCCTGA  
ACATCTGAAAGAGTTCACTGCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAAGGCTCAAACGCTTCA  
TCCAGCCCTACAGCTCAAATATCTGTACTCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA  
TTTGGCCAACACACTCCTTGTAAAGCTGAACAGGAACCTGAATCTAGCTATCCACCCAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAAATGAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAGTCTGAAAATGCAAAGAAATGGAGTAACGAAACATTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGGAAATTTCAGCTGGACCAATAACAACCTAACAGAGATTACCAAGGCTGGCTTACGGCTGCTGATGCT  
GCAGGAACCTCATCTAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAATTCAACTTAAGGTTAGATGATTCAAGGCTTCTGGCCTAAGCTTAAACTAAAC  
ACTGCACATTGGAAACAACAGACTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGCTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGAACGCAATCATGCTTACAAGGCAATGCAATTCAAAATGAAGAAACTGCAACAAATT  
GCATTAAATACATCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACTT  
TCAGAGCTTGTAAATGCCAGTTGTGCCCCATCTCAGCTGCTAAAAGGAAGAAGCATTTCGTTAGCCCAGA  
TGGCTTGTGTGATGATTTCCTAACCCCCAGATCACGGTCAGCCAGAAACACAGTCCGCAATAAAAGGTT  
CAATTGAGTTCTGCTCAGCTGCCAGCAGCTGATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAATTATGCACACCTCCGGCCAAAGGTGGCAGGGTGTGGAGTATACCAC  
CATCCTCGGCTGCGCAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTCTCATCTCAATTCACTTTGGTT  
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATCACCAAGGACCCCCATGGATCTCACC  
CCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGTTGGGACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGCACAGACTCCAGTGCACGGAGAGACGCATGATGATGCCAGGATGACGTGTTCTTATCGT  
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGC  
AACTCTGACTGTCCTAGAAACACCATCATTGGCGGCCACTGTGGACCGAAGTGTAAACCAAGGGAGAAACAGC  
CGTCCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAATGGACCAAGATGATAGCCCATTGGT  
AACCGAGAGGCACTTTGCAAGCAGGCAATCAGCTTGTGATTATGTGGACTCAGATGTCAGTGTGATGCTGGAA  
ATACACATGTGAGATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCCACTCCAAC  
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGCCACTGTGGGTGCTGATCATAGC  
CGTGGTTGCTGTGGTGGCACGTCACTGTTGGGTGGCATATACACACACAAGGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGTGGAGAACCAACTTGCAGCAGATATTCTAGTTATGTGTCATCTCAGGGACGTT  
AGCTGACAGGCAGGATGGTACGTGCTTCAGAAAGTGGAGGCCACCCAGTTGTCACTTCACTCAGGTGCTGG  
ATTTTCTTACACAAACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC  
CACAGATCTGTTCTTGTCCGTTTGGATCCACAGGCCCTATGTATTGAAGGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTTGCACTGCCAGCAAGAACAGTTAATGGACCACTATGAGCCAGTT  
CATAAAGAAAAAGGAGTGTACCCATGTTCTCATCCTCAAGAACATCTGCAACGGAGCTCAGTAATATATC  
GTGGCCTCAGATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAAATGAAAATCTGTG  
TCTAAACAAGTCTCTTAGATTAGTGCACATCCAGAGGCCAGCGTCGGTGCCTGAGTAATTCTTCTCATGG  
TACCTTGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGGCCATCAGATTGTCAGCC  
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTTGACTCTGGTCAGAGGAAGATGGGAAAGAAAGGAC  
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGTCAAGGACTCTCCAAATTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAGCTTAAACATACTACCTCAAGTGAACATT  
AAAGAGAGAAATCTTATGAAAATTGAGTTATGAATTAAAAGGATAAAAATGCTTATTATACAGAT  
GAACCAAATTACAAAAAGTTATGAAAATTGAGTTATGAATTAAAAGGATAAAAATGCTTATTATACAGAT  
TTTTTAACTTGTGTTATGAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTGTGAAATGAGTTACTAAAGCATTAAATACCTGCCATTGTGACCAATT  
TTAAATAGAAGTTACTTCATTATATTGACATTATTAATAAAATGTGCAATTGAA

## FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPAWE  
FCQKLSELDLTFNHLRLDDSSFLGLSLLNLTIGHNNRVSYIADCAFRLSSLKTLIDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILOQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPOQWAENNQSFVNASCACHPQLLKGRSIFAVSPDFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAKKDNEELLHDAEMENYAHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCMSNTLGETERGNVRLSVIPTPTCDSPQMTAPSLLDDG  
WATVGVIIIAVVCCVVGTSLVWVIIYHTRRRNEDCSITNTDETNLPADI PSYLSSQGTTLAD  
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDPFETYHTGCPDPRTVLMHDYEPSYIKKECYPCHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGTGGCTGCCTGCAAAATG  
AAGGATGGAGGACGCAGCTTCTGGAACCGAACGAACTGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAGAAATGAAA  
TAAACCAGAGTTAGACCCGGGGGGTGGTGTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCATTTTCTC  
TATAAGGAGAAAGTGGCCAAGGAGATATTTGGAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAAACT  
GGTGGTGGTGTCTTCTTGAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAATTGACGGATAATTGCGATTGGATTCTCATCAACCTCTTTTTAAAT  
TTTATTCCCTTGGTATCAAGATCATGCGTTCTTCTTAAACCACCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACGTGGTAATTCCAGAACGGACCAACACAGATAAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCCCTGCTGTGGTGC  
GCTGGCTCTCAACTCTTGTGGTGGCTGGTCTGGTGCAGACCTGCCCTCTGTGTGCTCGAGCAA  
CCAGTTCAGCAAGGTGATTGTTGGAAAAACCTCGCTGAGGTTCCGGATGCATCTCACCACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCCTCAAGCACTTGAGGCAC  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCATGGTCTGGCGAACCTCAACACTCTGA  
ACTCTTGACAAATCGTCTACTACCACCTCCGAATTGGAGCTTTGTATACTGTCTAAACTGAAGGAGCTGGTT  
GCGAAACAACCCATTGAAAGCATCCTTCTTATGCTTTAACAGAATTCCCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAA  
CATGTGCAACCTTGGAAATCCCTAACCTCACCCGCTCATAAAACAGATGAGCTGGATCTTCTGG  
TTTATCTGCCATCAGGCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT  
TCAAGTGAACGGAATGCCATTGACAACCTTCAGTCAGTCACTAGTGGAGATCAACCTGGCACACA  
ATTACTGCCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACA  
ATTACTGCCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACA  
TAACACTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTCGAACACAGC  
TAACACTCTCCAAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAACATTACT  
TACATGCTATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGA  
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCAGACACATGGGGCGTACA  
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACCTGTGCAAGATACAGGCATGT  
TTCCGGTGGAAACTACTGCTTCAGCCACCTGAATGTTACTGCA  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCA  
AGTGGTCAGTGGAGACCAATGTGACCACCTCTC  
CACCACCCAGTGA  
TGGGTGTTGGCCATCACACTCATGGCTGAGTGTGGTCA  
TCGGCAAAACCATCACCCCCAACAGGACTGTTGAAATT  
CATGGAAAGCCACCTGCCATGCC  
CTCTAAAGACAATGTACAAGAGACTCAAATTAAACATTACAGAGT  
GACAGTTATAAAAATGACACAAATGACTGGCTAAATCTACTGTT  
AAAAGAAAATTTATTAAACAGACAGACAAAA  
AAAAGAAAATTTATTAAACAGACAGACAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN  
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGAGTTGGCAGTTCTTCCCTCGCTGTTGGGGCA  
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACCGCACC  
GAGGGCGGGCGTCACCCCGGCTGGAAGTTGTGCCGGGCCAGCGCGCGCCGGCTGGGAGCTTCGGGTAGA  
GACCTAGGCCCTGGACCGCGATGAGCGCGCCAGCGCTCCGTGCCGCCGCCGGTTGGGGCTGCTGCTG  
GCCGTGCTGGGGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGTAGCC  
GAGCGCCCATGCCCACTACCTGCCGTCGCTCGGGACCTGCTGGACTCGCAGTCGAAGCGCTAGCGGTCTT  
CCCGAGCCACTCCGTCCTGGTCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTTCC  
ATGAGCCACCTCAAAGCCTTCGAGAAGTGAACACAATGAATTGGAGACCATTCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCTGGCTGGAAACAGGATTGTTGAATAACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATTTCAGAGCTCAGGACTTCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAAGGAACTGGGTATTGACAATTGGCAACACA  
CTCCTGTGTTAAAGCTGAACAGGAACCGAATTCAGCTATCCCACCCAAAGATGTTAAACTGCCCAACTGCAA  
CATCTGAATTGAACCGAAACAGATTAAATGTAGATGGACTGACATTCCAAGGCCCTGGTGTGCTGAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGAAATTG  
CAGCTGGACCATACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCTGCAGGAACCTCAT  
CTCAGCAGAAATGGCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAGCTCAGTGAGCTGGACCA  
ACTTCAATCACTTCAAGGTTAGATGATTCAAGCTCCCTGGCTTAAGCTTAAACTACACTGCACATTGG  
AAACACAGAGTCAGCTACATTGCTATTGCTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC  
AATGAAAATTCCGACTATTGAAGACATGAATGGCTTCTCTGGCTTGACAAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTACTGGTTGGATGATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTCCTTACAAGGCAATGCAATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAACA  
TCAAGCTTTGTCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCTTCAGAGCTTGT  
AATGCCAGTTGTCGCCCCATCCTCAGTGTCTAAAGGAAGAAGCATTGGCTTTAGCCAGATGGCTTGTG  
GATGATTTCCAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAGGTTCAATTGAGTT  
ATCTGCTCAGTGCAGCAGCAGTATTCCCAATGACTTTGCTGGAAAAAAAGACAATGAAACTACTGCATGAT  
GCTGAAATGAAAATTATGCACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTACACCACATCTGGCTG  
CGCAGGGTGGAAATTGCACTGAGGGAAATATCAGTGTGTCATCTCCAACTCATGGTTCATCTACTCTGTC  
AAAGCCAAGCTTACAGTAAATATGCTCCCTCATTCAACCAAGGCCCCATGGATCTCACCACCGAGCTGGGG  
ATGGCACGCTGGAGTGTGCTGTCGGGGCACCCAGCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC  
TTCCCAGCTGCACGGGAGAGACGCATGTCATGGCTGCTGTCAGTGTGATGCTGGAAATACACATGTGAG  
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTC  
CTAGAAAACACATCATTGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTCTACAGTGC  
ATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACTGGACCAAGATGATGCCATTGGTGGTAACCGAGAGGCAC  
TTTTTGCAAGCAGCAATCAGCTCTGATTATTGGAACCTCAGATGTCAGTGTGATGCTGGAAATACACATGTGAG  
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCCCTCAGTGTGATCCCCACTCCAACCTGCCACTCC  
CAGATGACAGCCCCATGTTAGACGATGACGGATGGCCACTGTGGGTGTCGTGATCATAGCCGTGTTGCTG  
GTGGTGGGACGTCACTCGTGTGGTGTGTCATATACACACAAGGGAGGAATGAAGATTGCAAGCATTAC  
AACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATGTGTCATCTCAGGGACGTTAGCTGACAGGCAG  
GATGGGTACGTGTCCTCAGAAAGTGGAGGCCACCAACAGTTGTCACATCTTCAGGTGCTGGATTTCCTTACCA  
CAACATGACAGTAGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTTGAGCTGCCACAGATCTGTC  
CTTGTCCGTTGGATCCACAGGCCCTATGTATTGAGGGAAATGTGATGGCTCAGATCCTTTGAAACA  
TATCATAAGGTTGCACTGCTTACCTGACCAAGAACAGTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG  
GAGTGCTACCCATGTTCTCATCCTCAGAAGAATCTGCGAACGGAGCTTCAGTAATATATCTGTCATC  
GTGAGGAAGCTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAATCTGTCATC  
TCTTAGATTGCAAAATCCAGAGGCCAGCGTGGTGCAGTAATTCTTCTATGGTACCTTTGAAA  
GCTCTCAGGAGACCTCACCTAGATGCTTACCTGAGCTGGACAGGCCATCAGATTGTCAGGCAAGAGCCTTT  
TTGAAAGCTCATTCTCCCCAGACTGGACTCTGGTCAAGGAAAGATGGGAAAGAAAGGACAGATTTCAGGAA  
GAAAATCACATTGTCACCTTAAACAGACTTAAAGAAACTACAGGACTCCAATTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACACTACCTCAAGTGAACCTTTATTAAAGAGAGAAT  
CTTATGTTTTAAATGGAGTTATGAATTAAAGGATAAAATGTTTATTATACAGATGAACCAAAATTAC  
AAAAAGTTATGAAAATTTCATCTGAAATGATATAAATCATGATTATTATGTTATGTTTATAATGCCAGA  
TTTATGCAAAAGTCTTACGTAATTAAATGATATAAATCATGATTATTATGTTATGTTTATAATGCCAGA  
TTTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTCACCTTTAAATAGAAGTT  
ACTCATTATATTGCACTTAAATAAAATGTGCAATTGAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIAKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRISSAIPPKMFKLPQLQHLELNRKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHLSRLDDSSFLGLSLNLTIHGNNRVSYIADCAFRLGSSLKTLDLKNNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSIKKAKFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLCDQLKWLHQWVAENNQSFVNASCAGPQLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNEELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYCTAQNSA  
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPMLPSFTKTPMDLTIRAGAMA  
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRLSIVPTPTCDSPQMTAPSLODDGWA  
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO  
DGYVSSESGSHHQFTSSGAGFFLPQHDSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDFETYHTGSPDPRTVLMHDYEPSYIKKKECYPCHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCCACTGACTTGAATGGAAGGAGCCCGAGCCCGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCGGCTGTGGGGCGCCGCTCGCGCCGGGGCGCAGCAGGGAAAGGGAAAGCTGTGGTCTGCC  
CTGCTCCACGAGGGGCCACTGGTGTGAACCGGGAGAGGCCCTGGTGTCCCTATCCCTCTTATATA  
GAAACCTTCCACACTGGAAAGGCAGCGCGAGGAGGGCTCATGGTGAAGCAAGGAGGCCGCTGATCTGCAG  
GCGCACAGCATTGAGTTACAGATTACAGATACCAAAATGGAAGGCAGGAGGCAGAACAGCCTGCCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGCACCCCTGCAGGCACCATGGCCAGAGGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCGGTGAGGGGCCAGGATTGGCCGAA  
GTGGCGGCCACAGCTGAGCCCCGAAGAGAACGATTGCGGAGGAGGCCGGTGTGGTACTGAGCCCTGAGG  
AGCCCAGGGCTGGCCAGCCCGGTCAGCTGCCCGAGACTGTGCCCTGGCCAGGAGGCCGTCGTGAGCTGTG  
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGAGAACACACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACCGGCTGGAGACACTGAAACCTGCAAAACACCGCCTGA  
CTTCCCAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTAACCTGGCCAAATAAACAGC  
TGACCTTGGCACCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTGTGCCAACTATCTACCAAGATCT  
ATGGGCTCACCTTGGCCAGAACCAAACCTGAGGTCTGTGACCTGCACAAACAAACAGCTGGCAGACGCCGGG  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGCTGAGGTCTCATCTGTGCCAGCAACCTCTGCGCACGTG  
CCAAGCACCTGCCCTGCCCTGTACAAGCTGACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCCT  
TCAGCGAGCTGAGCACGCTGCCAGCTGGCAGACTACCTGAGAACAAACTACTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTGCAAGAACAAACCTGTCTGGTCCAGCTGGCTG  
CGCGCAGCCTGGTGTGCTGCACTTGGAGAACAGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGTGCTGCAAGCAACCAAGCTGCCAGGCACTGGCCTTCCAGGGCC  
TCAAGCGGTGCAACGGTGCACCTGTACAACAAACGCGCTGGAGCGCGTGGCAGTGGCTGCTGCCAGTGGCTG  
GCACCCCATGATCTGCACAACAGATCACAGGCATTGGCGGAAGACTTGTGCCACCAACTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACCAGCCACAGGTGCAACGGCATTCCGCAAGCTGCGCTGCTGC  
GCTCGTGGACCTGTGGCAACCGGGTGCACACGCTGCCACCTGGGCTGCCCTGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCAGAGGGCGCTGGCGGGCATGGCTAGCTGCCAGTGGCTGAGCTGTACCTCA  
CCAGCAACCGACTGCGAGCCGAGGCCCTGGGCCCCCGTGCCTGGTGGACCTGCCATCTGCAGCTGCTGGACA  
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACCTGAGTACCTGCAAGAACACA  
AGATTAGTGCCTGGCCCAATGCCCTGACTCCACGCCAACCTCAAGGGATCTTCAGGTTAACAAAGC  
TGGCTGGGCTCCGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGCAACT  
TAGAGTTGGTGCACATTCCAAGGACCGTGGCCCTGGGAAGGAAAGGAGGAGGAGGAGAACAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTACAAGGTGATGAGATGTGACCTAGGATGATGGACCGCCGACTCTTTCTGC  
AGCACACGCCCTGTGCTGTGAGCCCCCACTCTGCCGTGTCACACAGAACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCAGGGCACAGCATG  
ACACACATCACACCCCTAAACACCCAGCTCAGGCCACACACAACCTACCCCTCCAAACACCAAGTCTGTG  
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAAAGGTCTGCCCTGGCACACACAGGCCACCC  
TTCCCTCCCTGCTGACATGTGATGCTGATGCAACACACACACACATGCAAGTCATGTGCGAA  
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTGCCAGGCCAGAACATGCCATAGCAGCTGCCGTG  
GTCCATCTGCTGCCCTGGAGAACAGACAAAGGGTATCCATGCTGTGGCCAGGTGCTGCCACCCCT  
GGAACCTACAAAAGCTGGTTTATTCTTCCATCCTATGGGACAGGAGCCTTCAGGACTGCTGCCCTGGC  
TGGCCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTCCAATGGGAAGGCCAGTGGAGGCAGGATGGAGAGGCCCTGGGTGCTGGGGCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTCAGGCCCTGTGGGGAGTCCGGGTGCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAA  
CTAAAGCTGATTTCTGTTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENFAEEEPLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFLTNLYLANNK  
LTLPAPRFLPNALISVDFANYLTQIYGLTFGQKPNLRSVYLHNNKLAAGLPDNMFNGSSNV  
EVLISSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTD  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPVRVRLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDASFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCGCGCCTCGCCGCTGTCCCTCCGGGAGCGGGCAG  
CAGTAGCCCGGGCGGGAGGGCTGGGGCTCCCTCGAGACTCTCAGAGGGCGCTCCCATCGCGCCACCA  
CAACCTGTTCTCGCGGCCACTCGCCTCGCGCCCCAGGACCCGCTGCCAACATGGATTCTCTGGCGCTGGT  
GCTGGTATCTCGCTCACCTGCAGCGGCCGAGTCGACGGGAGGTGGCCAGGCAAATAGTGTCACTGAT  
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGCTCGCCAGTCTTGGGACAGTGTCA  
TGTGTGCCAACACGATGCAAACATGGTAATGTATCGGCCAACAAAGTGAAGTGTCA  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGCCCTGAAGCCCCGGCCCTGTAAGCAGGGCATGAACACTTA  
CGGCAGCTACAAGTGTACTGTCACGGATATATGCTCATGCCGATGGTTCTGCTCAAGTGCCTGACCTG  
CTCCATGGCAAACGTCACTGGCTGTGATGGTAAAGGACAAATACGGTGCAGTGCCTGCCATCCCTGGCCT  
GCACCTGGCTCTGATGGGAGGACCTGTAAGTGTGATGAAATGTGCTACAGGAAGGCCCTGCCCTAGATT  
TAGGCAATGTGCAACACTTTGGGAGCTACATCTGCAAGTGTGATCAAAGGCTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTCAATGACATAGACGAATGCTACTGGTCAGTATCAGTGCAGCAGCTTGCTGATGTTATAA  
CGTACGTGGGCTCTACAAGTCAAATGTAAGGATACAGGGTGTGACTGACTTGTGTTATCCAAA  
AGTTATGATTGAAACCTCAGGCTCAAATCATGTAACAAAGGAAATGGTACCAATTAAAGGTGACACAGGAA  
TAATAATTGGATTCTGATGTTGGAAGTACTGGTGGCTCGAAGACACCATATATTCCCTCATCATTACAA  
CAGGCCACTCTCAAGCCAACAACAGACCTACACCAAGCCAACACCAATTCTACTCCACCACCA  
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACGGACTGACA  
ACCACTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTAGAAACCCAGGG  
AGATGTGTTCACTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACTGGGACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAGGCCAGG  
GGGAAAGCTGCACTGGTGTACCTCTGGCCGCTCATGCATTAGGGGACCTGTGCCTGTCATTGAGGCA  
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCTGGAGCAGCC  
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTGCGAGGGCTGACATCAAGAGCGAATACA  
AAGATGATTAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGAAG  
AGAAAGACTGAGGGGCAACACCATTGATGGTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCACCAGCTG  
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTTCTGGCAGG  
GCCATTGTTAGAATACTTCATAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAGGAAATTAGA  
AAAAAATTGTCATTTAAGATGGTAAAGATGTTCTACCAAGGAAAAGTAACAAATTATAGAATTTC  
AGATGTTTGATCCTACTAGTAGTATGCACTGAAAATCTTAGAACTAAATAATTGGACAAGGCTTAATTAGG  
CATTTCCCTCTGACCTCTTAATGGAGAGGGATTGAAAGGGGAAGAGGCCACAAATGCTGAGCTACTGAAATA  
TCTCTCCCTTATGGCAATCTCAGTATTAAAGAAAAAGGAAACTATTATTC  
AGATATTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGGC  
TTTCATTGTCATGGATGTTCAAGATTTTTTTTAAGAGATCCTCAAGGAACACAGTTCAGAGAG  
ATTTTCATGGGTGCATTCTCTGCTTCGTGTCAGAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC  
ACACCGGCAGACCTTCTCACCTCATCAGTATGATTAGTTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTGAACAATAGGTACAATAGAAGGTCTCTGTCATTAAACCTGTAAGGCAGGGCTGG  
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATGGCTGAGATCCATTAAATGGTTCA  
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTACTTTCGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTAAATGTTT  
CTAAAATAAAATGTTAGTGGTTCCAAATGGCCTAATAAAAACAATTATTGTAATAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCOPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDRTCDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA AASTPPGGITVDN  
RVQTDPQKPRGDVF SVL VHS CNFDHGLCGWI REKDNDLHWEPI RD PAGGQYLT VSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACTTTCTTGCACAGGTGCTGGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA  
ACAATGCCAAATACTTACTGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACCC  
AACACAAGTCACCATGATGCCACCAATGCATCTGTCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACTCTATCTGCCAGTCA  
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAGCCAGTGGTGCAGATTCATCCTCCCT  
CTGGGGCTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGACTCGG  
CTAGCTTACCAATGGCTAAAAATGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT  
GCCTGGTGAGGAACCTGTCAGTGAAATGGAAGTGAATTCATTATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTGCTAGAAGTT  
GCATCTGAGAAAGTAGCCAGAACAGAACATGGACTATGTTGCTGCTTACAACACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTACATCCTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATACTGGAATATCACTATTGATT  
ATATCCATGTCCTCTTCTATGGAAAAATATCAACCTACAAAGTTATAAAACAGAA  
ACTAGAACGCCAGAACAGAACATACAGGAAAGCTCAAACATTTCAAGGCCATGAAGATG  
CTCTGGATGACTCGGAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTTGATCGGGCAAGATTGCACTAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACTTCATGG  
GCTAAACAGTACATTGAGTGAAGAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATTCTTTACA  
TGCAGAACAGGAAACTTATGCAAATTGAACTGCACTGCAGGTTTCAGCATATACACAAATGTCTT  
GTGCAACAGAAAAACATGTTGGGAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGAACAGGGTTCTCATAAGTTGTATGAAATATCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCACCTACAAA  
TGTGGAAACTTACATTGTCGATTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTGTTATTGTACAA  
CAAAGTAATAAGGATGGTTGTCACAAAAACAAACTATGCCCTCTTTTTCAATCACC  
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGCTTTAAAAAA

## FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDPPVTKPVQIHPGSAVEYVGNMTLCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV  
YEVIQHIPAAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGGCCGAAATGGCGCCCTCCGGGAGTCTTGCAGTCTCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGTCCCTGGACGCACGGCGGAGCAACGTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATGAGAATTTATGCCCCGTGGTGCCTGCT  
TGTCAAAATCTCAACCGGAATGGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGTAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG  
GTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC  
AGATTGCCTTGTCCTTCAAAAAGGCGCAGACACAGCCATACCCATACCCCTCAAAAAAAT  
TATTATCAGAATCTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGATGAAGAA  
GATGTTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC  
CATAAAGACAACGCTCTGGTCCATCATTGCCACAGATAAATCTAGTTAAATTATAG  
TTATCTTAATATTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGAAATTGCAGGGTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAATATGATTAAAGCACAGTATGATG  
GTTAAATAGTCTCAATTGGAAAATCGGCCAGCAATAAGATTATGTATATTGT  
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCATTAT  
TGAGGTATTAAAGAAGATTTTAGAGAAAATTTCTCATTGATATAATTCTCTG  
TTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGATTTCAGTGACAATTCTGGTCTTTAGAGGTATATTCAAATTTCCTTGT  
ATTTTTAGTTATGCAACTAATAAAACTACCTTACATTAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTGATT  
CAACAAAGTTGATTCTCTGTATTTCTTACTTACTATGGTTACATTTTATTGTT  
CAAATTGGATGATAATTCTGGAAACATTTTATGTTTAGAAACAGTATTGTTGTT  
GTTCAAACGTGAAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGAATTAAATT  
TTGGCCACTTTTCAGATTTCATCATTCTGCTGAACCTCAACTGAAATTGTTTTT  
TTTCATTGATGTGAAAGGTGAAACATTCTGATTGTCATTCTACTCAGGAAAAAG  
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAAG  
CATCTTCTGTATATGCTTAATGTATTGTCCTCATATACAGAAAGTTCTTAATTGAT  
TTACAGTCTGTAATGCTGATGTTAAAATAAAACATTTTATATTGTTAAAAGACAA  
ACTTCATATTATCCTGTGTTCTTCTGACTGGTAATTGTTGAGGATTCACAGGTAAA  
GTCAGTAGGATGGAACATTAGTGTATTCTAAAGAGCTAGAATACATAGTTT  
CACCTTAAAGAAGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGCCCCCTTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG  
TATCGTAATATACAAGTTCTTAAAGCCCTCTCTTCTAGAATTAAATTGTAACCT  
AAAGAGTTGGATGTGTAACCTGATGCCTAGAAAATATCCTAAGCACAAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGA  
PWTGHRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNI  
AKV  
DVTEQPG  
LSGRFI  
ITALPTIYHCKDGEFRRYQG  
PRTKKDFI  
NFISDKEWKSIEPVSSWFGPGS  
VLMSSMSALFQLSMW  
IRTCHNYFIEDLGLPVWGSYTVF  
AL  
ATLFSGLLLGLCMIFVADCLC  
PSKRRPQPYPYPSKKLL  
SESAQPLKK  
V  
EEEQEADEEDV  
SE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## FIGURE 115

CGAGTGTCCAGCTGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTGTGACACTTCCCTGTGACCATGAAACTCTGGGTGTCTGC  
AAGTCCTGCCAGAGCAGTGTGACACTTCCCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCTGGTTGGTGTCCCTGAGCTGTGAGGCCAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTACCCCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCTCGCTGGAGGACCTGTCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGAGCAGCTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATAACGGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCGCTGCTC  
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAACGACTGAGCTAGCAACCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG  
GAGGGTGTCAAACGTACACCCGTAGACAGAACAGAGGCTTCTGTAGGTACCAACATGGCAA  
CAGGGCCCCACAGCTGCTATTGCCCTTCAAAGAGGAGGACGAGTGGACAGCCCGACA  
TCGTCAGGTACTACCGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATCGCAAA  
CCTAAACTGCACGCCACCGTCTGATCCAAGACAGGAGTCCTCACTGTCGCCAGCTA  
CCGGGTTTCAAAAGCTCTGGCTAGAGGAAGGATGATGACCCCTGTTGTGGCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTGACAGCGG  
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGT  
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC  
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTGTGGATCAACAGAACAGTGACTGACATCCTTCTGTCTTCCCTCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTCATTAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA  
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAAGTGAACCAAAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAATGTCCCTACCAGAAAAAA

## FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFF  
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYHTV  
LWMEQVLKOLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDPYPERDVYESLCRGEVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMDSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHDFSR  
RRPFDGGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTACTCCTCCTTTAGTGGAAAGACAGACCATATCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTGGCTGGGGTTAGTCCGACACCTTCACAGTGAAGAGCAGGCCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTTGGGATGCTGGCTTGGAAAGCCAGCAGGGCTTGCTCTGCTTGGCCTCATTGACCC  
CAGGTTCTCTGTTAAAAGCTACTACTGGCCTGGTGCCTCAATCATTGATCCTTGAGGCTGTGC  
CCTGGGCACCCACCTGGCAGGGCTTACCAACCAGCAGACTGAGCTCCCTGTTGCTCTGCTGGCCAGCGCTTC  
CCCTCATCTTAAAGGCTGCTCTGGGCTGAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCAGGCTGTAGGGAGCGAGGAGGGCACAGAATCCAGATTGAGAGCTGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGATTGTCCTACTACAGGGACCCAAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGCCTCCGTGAGCGGTTGCTGGCTGTGACCTCCGAGCTACACTGTCCA  
CTTGGCCGTGGCTGTAACCGTACGGTGGCCATCACTTCCCTCGTTACTCTACCTTCACTGGCAGCGGGGG  
CCCAGGCTCCAGCAGGGATGCGAGTGGTGTCTCATGGGATGAGCGGCCCTGGCTCATGTGAGAGACCCCTGC  
GCCACCTTCACACACACTTGGGCGACTACGACTGGTCTTCATCATGCGAGATGACACATATGTGAGGCC  
CCCAGCCTGGCAGCCCTGGTGCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTATTG  
GCGCAGGCAGCAGGCCGGTACTGTCATGGGGCTTGGCTACCTGTCAGGAGTCTCTGCTTCGTCTGC  
GGCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCCGTCTGACGAGTGGCTGGACGCTGCCATTG  
ACTCTCTGGCGCTGGCTGTCTCACAGCAGGGCAGCAGTATGCTCATTTGAACGGCAAAATAGGG  
ACCCAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTCGCCGTGACCCCTGCTCCGAAGGTACCCCTCATGT  
ACCCGCTCCACAAACGCTCAGCGCTCTGGAGTTGGCAGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGGTGGCTCCCTGCTCCTTCA  
CACACACTCTCGCTTGGAGGTGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTCAGATGGG  
CTCCAAAGTGGCCACTACAGGGGCTAGCAGGGGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGGGCTATCAGCCCCGCTGCGCTTCCAGAACAGCAGCAGACTGCTCAACGGCTATGGCGTTCGACCCAGCAC  
GGGCATGGAGTACACCTGGACCTGCTTGGAAATGTCAGACAGCGTGGCACGGCGGGCCCTGGCTCGA  
GGTCAGCCTGCTGCGGCCACTGAGCGGGTGGAAATCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGTTCTCGAGGGCTTGCAGCCAATGTCC  
TGGAGCCACGAGAACATGCTCATTGCTCACCCCTGTTGCTGGTCTACGGCCACGAGAACGGTGGCGTGGAGCTCAG  
ACCCATTCTGGGTGAAGGCTGAGCAGGGAGTTAGAGCAGGGTACCTGGACGGCTGGCTGGC  
CTGTGCGAGCAGAGGCCCTCCAGGTGCGACTCATGGACGTGGCTCGAACAGAACGACCCCTGTGGACACTCTCT  
TCTCCTTACACCCTGTTCCAGGAGTTCAATCCTGCCCTGTCACCAAGAGATCACCCCCAGGGCCCC  
GGCAGGCCCTTCCAGTCCATTCCAGGAGTTCAATCCTGCCCTGTCACCAAGAGATCACCCCCAGGGCCCC  
CGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGCTCTATAGGGGGAGATTG  
ACCCGCAGGCTTCTGCGAGGGCTGCTTCAACAGCTGACTACCTGGCGGCCAGGCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTCTCCGTTCTCAGGGCTCC  
ACCTCTTCTGGCCGTAGAGCCAGGGCTGGTGTGAGAACGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
AACTCTACCCACCGCTGCCGCTCAAGAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCTGGGGCCCTAACCTCATACCTTCTTGTCTGCCTCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGATTTTAAATATGAAAATGTTATTAA  
ACATGTCTCTGCC

100 70 40 10 5 2 1

## FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPONPDSRARLD  
QSDEDFKPRIVPYRDPNPKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQQAQIRNLTVLTPEGEAGLSPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTL DLLECVTQRGHRRALARRVSSLRPLSRVEILPMPYVTEATRVQLVLPLL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVKHPVDTLFFLTWTRPGPEVLNRCRMAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEFCYNAADYLAA  
RARLAGELAGQEEEALEGLEVMDFVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAGQLAMALFEQEQANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGC~~GG~~CAACGTGAGAGGAAACCGTGC~~GG~~CTGCGCTT~~CC~~GTCCCAGCC  
GTTCTAGAC~~GG~~AAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTC  
GAGGATGAGCGATGGAGCTCAGTAAGAGCTTCGAGTACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTCTTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACA  
GTTCTTCCTGCACGCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAACTGGAGACCTGAAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACTCAA  
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTAGGCATTGGCATATTTC  
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGAGTAGTAACATACATATCAA  
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGGTTTTCTTAAAGAATAATAATTGCAAATAACTATT  
TGTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT  
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT  
AAAAAATTAAACAGGTCTTAGCCTCTAACATGAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTCTAGCTGTGTGTTCCCTTACTTCTAACACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

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## FIGURE 122

MNSSKSSETQCTERGCFSQMFLLWTVAGIPILFLSACFITRCVVTFRIFOTCDEKKFQLPEN  
FTELSCYNYGGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDTPLTKSLSFWDVGEPNNIATLEDATMRDSS  
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

GGGACTACAAGCCGCCGCCGCTGCCGCTGGCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCCTCGGCTGACTCTTCTGCTGCTTCAAGGGCTGCCGTATAGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAACGTCTGCATCATTACGGATTGCG  
AGACAAGTGAACCCAGGATCGAGTGAAGAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGTCGTGAGAAATACTGGGAAGACATCCCTGAAGATCTGAGTACACGGAGAG  
ACTCAGCCCTTATCGCTGTAGGTGCTCGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCAATCCAGATTGCAATTCTCTTCACTAAACTCTGAAAACAGGCACTTGGTGTTCACTGCTG  
TTCACAAGGAGACTCTGGGAGTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGGAAATTATTGGGGGGTCTGGTTGCTGTACTGGCCCTGA  
TCACGTTGGCATCTGCTGTGCATACAGCTGGTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTG  
TGATCTGAGACCCGCGGTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCAGAGACTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAGCCTTCGTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAACACTGGGTGCGTTACTGAGTTGGTCTTAATCTGTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTGCTCACGTAAACGCCGTCTGGGCGCTGTGAAGCCAGCATGTCACCACGGTC  
CAGCAGCCACGACAGCACATGTGAGATGGCAGGGTGGCAGCACCAGCAGCGCATCCGGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTACTTCATCGGCCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGACTGTCATTGTTGAGAAGCTTTGGATCAGCATTGTTGAAACAAACAAAATCAGGAAG  
GTAATTGGTGTGAGGAGGGACTTGGCTGAGGAACCTGCTGTCAAACAGGGTGTCAAGGATTTAAGGAA  
ACCTCGTCTTAGGCTAACGTCTGAAATGGTACTGAAATATGCTTTCTATGGGCTTGTATTATTTATAAAATT  
TACATCTAAATTGGCTAACGGATGTTGGATTATTGAAAGAAATTCTATTAAACTGAAATATATTGT  
CATACAATGTTAAATAACCTTTTAAAGGTTCAACTTAAGGTAGAAGTCCAAAGCTACTAGTGTAAAT  
TGGAAATATCAATAATTAGAGTATTTTACCAAGGAATCCCTCATGGAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTAGCCTTTCACAGGGAACTCATACTGTCACACATCAGACCATAGTGCTTAGGAAACCTT  
AAAAAATTCCAGTAAGAATGTTGAAATCAGTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGAAC  
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACGCCTCAGATGTACATACAGATG  
CCAGTCAGCTCTGGGTGCGCCAGGCGCCCCGCTCTAGCTACTGTTGCCCGTGTGCCAGGAGGCC  
GCCATCCCTGGGCCCTGGCAGTGGCTGTCCAGTGAGCTTACTCACGTGCCCTGCTCATCCAGCACAGC  
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCAGCTTGGCTCCTGTAACAGACCTCT  
TTTGTTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTTTTTTTAAGTTGTTAAATTATTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCAAATCAAGTCTGCAAGTACAATAACATTTTAAAGAAAATGGAT  
CCCACTGTTCCCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGCGATTTCAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGGCCAGGTGAAAGGCCGGAGGAAAG  
TGAAACGCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTCTATCGGCCGGAGACACTGCTCCCATT  
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC  
GCCGTGCTGGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCC  
GAATGGGCTCTCACTACTCACCTGTTCTCAGCTTCCAGTGTCTGGTTTTTATACATTGACAGCTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGGCGCAGGCCCTGCCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCTGGATGCTTAGCATGCAAGTC  
CCTCCCATGCCACCTGGTAGAGAGGGATGGCTCCACCCCTCAGCGTTGGGATTACGCTCCAGCCTCCT  
TCTTGGGTCTAGTGATAGGGTAGCCTTATTGCCCTCTTATACCTAAACCTCTACACTAGTGC  
TGGAAACAGGTCTGAAAAAGTAGAGAGAACGTAAGAGTAGCTGGAGTAGCTGCCATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTTATAAAAGCTTCAAAAAACCCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267